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Hnies, J.
09/272809
Seq. ID 9

****

MPSRCH (TM)

****

Release 3.1A John F. Collins, Biocomputing Research Unit.

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Sep 13 14:25:32 1999; MasPar time 9.62 Seconds
433.103 Million cell updates/sec

Tabular output not generated.

Title: >US-09-272-809-9
Description: (1-196) from US09272809.pep
Perfect Score: 1458
Sequence: 1 KLAVRAISRLQSLPGGDIGA.....QAFGLQLQMELQLASQLAEK 196

Scoring table: PAM 150
Gap 11

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39

Statistics: Mean 31.852; Variance 133.240; scale 0.239

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1019	69.9	1142	32	W50145	Mesotaenium caldarior	7.36e-89
2	837	57.4	1129	32	W50144	Oat phytochrome A apo	1.58e-70
3	403	27.6	748	32	W50143	Cyanobacterial phytoc	1.50e-27
4	104	7.1	353	2	P70204	Sequence of human inh	2.65e+00
5	101	6.9	91	2	P70852	Sequence of inhibin b	4.51e+00
6	94	6.4	621	37	W73007	Cobra venom protease	1.53e+01
7	91	6.2	351	2	P70201	Sequence of porcine i	2.57e+01
8	90	6.2	613	37	W73009	Cobra venom protease	3.04e+01
9	90	6.2	621	37	W73013	Cobra venom mocarhagi	3.04e+01
10	89	6.1	638	1	P81326	Human growth hormone	3.60e+01
11	87	6.0	236	31	W28089	Amino acid sequence o	5.05e+01
12	87	6.0	746	20	W03178	Human poly-immunoglob	5.05e+01
13	87	6.0	1873	1	P95645	Rabbit seletal muscle	5.05e+01
14	87	6.0	1873	22	W18390	Rabbit calcium channe	5.05e+01
15	87	6.0	1873	26	W37711	Rabbit skeletal calci	5.05e+01
16	87	6.0	1873	13	R73055	Rabbit skeletal calci	5.05e+01
17	86	5.9	317	17	R85862	WD-40 domain-contg. h	5.96e+01
18	86	5.9	317	17	R85867	WD-40 domain-contg. h	5.96e+01
19	86	5.9	317	17	R85850	Receptor of activated	5.96e+01
20	86	5.9	337	26	W29215	Human Pax9 gene produ	5.96e+01
21	86	5.9	637	1	P92108	Human growth hormone	5.96e+01
22	86	5.9	638	28	W33394	Human growth hormone	5.96e+01
23	84	5.8	195	32	W44870	Cytochrome P450IId6 f	8.31e+01
24	85	5.8	400	2	R12131	ORF 3 of IgG light ch	7.04e+01
25	84	5.8	497	18	R93183	Human cytochrome P450	8.31e+01
26	84	5.8	497	18	R93182	Human cytochrome P450	8.31e+01
27	84	5.8	497	13	R72377	Human auxillary cytoc	8.31e+01
28	84	5.8	497	13	R72375	Human auxillary cytoc	8.31e+01
29	84	5.8	497	13	R72376	Human auxillary cytoc	8.31e+01
30	84	5.8	497	13	R72378	Human auxillary cytoc	8.31e+01
31	84	5.8	497	17	R81462	Human derived cytochr	8.31e+01
32	84	5.8	497	32	W44869	Cytochrome P450IId6.	8.31e+01
33	84	5.8	497	18	R93184	Human cytochrome P450	8.31e+01
34	84	5.8	497	18	R93185	Human cytochrome P450	8.31e+01
35	85	5.8	671	11	R61135	Delta-pyrroline-5-car	7.04e+01
36	85	5.8	671	23	W24386	Delta1-pyrroline-5-ca	7.04e+01
37	85	5.8	703	29	W47389	Rice delta-1-pyrrolin	7.04e+01
38	84	5.8	752	7	R38153	Acetobacter diguanyla	8.31e+01
39	84	5.8	828	3	R13905	Rabbit ATHERO-ELAM.	8.31e+01
40	84	5.8	4630	23	W19629	Streptomyces venezuel	8.31e+01
41	83	5.7	356	22	W20895	H. pylori transporter	9.80e+01
42	82	5.6	223	33	W61218	Streptococcus pneumon	1.15e+02
43	82	5.6	849	38	W82397	Human UBP protein #3.	1.15e+02
44	82	5.6	859	10	R53268	120-128 kilodalton an	1.15e+02
45	82	5.6	1181	18	R91307	Helicobacter pylori T	1.15e+02

ALIGNMENTS

RESULT 1
ID W50145 standard; protein; 1142 AA.
AC W50145;
DT 28-AUG-1998 (first entry)
DE Mesotaenium caldariorum phytochrome apoprotein.
KW Phytofluor; fluorescent label; phytochrome; green alga.
OS Mesotaenium caldariorum.
PN WO9805944-A1.
PD 12-FEB-1998.
PF 01-AUG-1997; U13529.
PR 02-AUG-1996; US-023217.
PA (REGC) UNIV CALIFORNIA.
PI Lagarias JC, Murphy JT;
DR WPI; 98-145711/13.
PT Adducts of apoprotein polypeptide and chromophore as label,
PT particularly for bio-molecules - used as fluorescent markers in
PT immunoassays, nucleic acid hybridisation, detecting protein-protein
PT interaction etc., are stable with high molar absorption
PS Example 2; Page 64; 87pp; English.
CC This polypeptide comprises a phytochrome of the green alga
CC Mesotaenium caldariorum. The invention provides a new class of
CC fluorescent protein adducts (phytofluors) that are generally
CC suitable for use as fluorescent markers. They comprise a protein
CC component (an apoprotein) and a bilin chromophore such as
CC phycoerythrobilin. Preferred apoproteins are obtained from plants,
CC e.g. oat (see W50144), from green algae, or from cyanobacteria (see
CC W50143). Truncated apoproteins consisting of the N-terminal
CC chromophore domain are especially preferred. Recombinant
CC apoproteins assemble spontaneously with the bilin chromophore.
CC Claimed compositions comprise a protein, glycoprotein, antibody or
CC nucleic acid to be detected linked to the phytofluor. They are used
CC in assays for detecting the other member of a specific binding pair,
CC e.g. immunoassay of antigens, immuno-histochemical labelling, as
CC nucleic acid probes for Southern blotting, for identification of
CC manufactured products, also to detect protein-protein interactions,
CC including studies on intracellular protein localisation and
CC identification of transfected cells. The phytofluors make ideal
CC fluorescent markers because they have a long wavelength absorption
CC maximum and high molar absorption coefficient, and are stable to
CC light and pH.

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SQ   Sequence   1142 AA;

  Query Match           69.9%;  Score 1019;  DB 32;  Length 1142;
  Best Local Similarity  69.5%;  Pred. No. 7.36e-89;
  Matches   146;  Conservative   28;  Mismatches  22;  Indels  14;  Gaps   3;

Db    203 klaakaisrlqslpggdigllcdavveevreltgydrvmaykfhedehgeviaeirrsdl 262
          ||| :|||||||||||||| |||:|||:|: |||||||| | ||||:||||::|||||||
Qy      1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL 60

Db    263 epylglhypatdipqaarflfmknrvriicdcsappvkviqdptmkhpislagstlrgvh 322
          ||||||||||||||||||||: ||||:||||:| ||||:|   :|:|: |  ||||: |
Qy     61 EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120

Db    323 gchaqymanmgsvaslvmaviindnsseegataaggilhkgrklwglvvchhsspryvpf 382
          |||:|||||||||||| :|:::: :   :   ::       |||||| || |||||||
Qy    121 GCHTQYMANMGSVASLALAIVVKGK---D---SS--------KLWGLVVGHHCSPRYVPF 166

Db    383 plrsaceflmqvfglqlnmevelssqlrek 412
          ||| ||||||| ||||| ||::|:||| ||
Qy    167 PLRYACEFLMQAFGLQLQMELQLASQLAEK 196


RESULT    2
ID   W50144 standard; protein; 1129 AA.
AC   W50144;
DT   28-AUG-1998  (first entry)
DE   Oat phytochrome A apoprotein.
KW   Phytofluor; fluorescent label; phytochrome A; oat.
OS   Avena sativa.
PN   WO9805944-A1.
PD   12-FEB-1998.
PF   01-AUG-1997; U13529.
PR   02-AUG-1996; US-023217.
PA   (REGC ) UNIV CALIFORNIA.
PI   Lagarias JC, Murphy JT;
DR   WPI; 98-145711/13.
PT   Adducts of apoprotein polypeptide and chromophore as label,
PT   particularly for bio-molecules - used as fluorescent markers in
PT   immunoassays, nucleic acid hybridisation, detecting protein-protein
PT   interaction etc., are stable with high molar absorption
PS   Example 1; Page 63; 87pp; English.
CC   This polypeptide comprises phytochrome A (PHYA) of oat.  A method
CC   for the efficient purification of recombinant PHYA from
CC   Saccharomyces cerevisiae using a C-terminal epitope tag is
CC   provided.  The invention provides a new class of fluorescent
CC   protein adducts (designated phytofluors) that are generally suitable
CC   for use as fluorescent markers.  They comprise a protein component
CC   (an apoprotein) and a bilin chromophore such as phycoerythrobilin.
CC   Preferred apoproteins are obtained from plants, e.g. oats, from
CC   green algae, e.g. Mesotaenium caldariorum (see W50145), or from
CC   cyanobacteria such as Synechocystis (see W50143).  Truncated
CC   apoproteins consisting of the N-terminal chromophore domain are
CC   especially preferred.  Recombinant apoproteins assemble
CC   spontaneously with the bilin chromophore.  Claimed compositions
CC   comprise a protein, glycoprotein, antibody or nucleic acid to be
CC   detected linked to the fluorescent adduct.  They are used in assays
CC   for detecting the other member of a specific binding pair, e.g.
CC   immunoassay of antigens, immuno-histochemical labelling, as nucleic
CC   acid probes for Southern blotting, for identification of manufactured
CC   products, also to detect protein-protein interactions, including
CC   studies on intracellular protein localisation and identification of
CC   transfected cells.  The phytofluors make ideal fluorescent markers
CC   because they have a long wavelength absorption maximum and high
CC   molar absorption coefficient, and are stable to light and pH.
SQ   Sequence   1129 AA;

  Query Match           57.4%;  Score 837;  DB 32;  Length 1129;
  Best Local Similarity  60.7%;  Pred. No. 1.58e-70;
  Matches   128;  Conservative   32;  Mismatches  36;  Indels  15;  Gaps   4;

Db    201 klaakaiskiqslpggsmevlcntvvkevfdltgydrvmaykfheddhgevfseitkpgl 260
          ||| :|||::|||||| :  ||:||| :|  |||||||| | |||||||:|| |||:: |
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Qy      1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL 60

Db    261 epylglhypatdipqaarllfmknkvrmicdcrarsikvieaealpfdislcgsalraph 320
          ||||||||||||||||||:||: |:|||||| | ::||:::| |   : |  |:|||||
Qy     61 EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120

Db    321 schlqymenmnsiaslvmavvvneneeddeaeseqpaqqqkkkklwgllvchhespryvp 380
          :|| ||| || |:||| :|:||: :   |   |   :      |||||:| || ||||||
Qy    121 GCHTQYMANMGSVASLALAIVVKGK---D---S---S------KLWGLVVGHHCSPRYVP 165

Db    381 fplryaceflaqvfavhvnrefelekqlrek 411
          |||||||||| | |::::  |::|  || ||
Qy    166 FPLRYACEFLMQAFGLQLQMELQLASQLAEK 196


RESULT    3
ID   W50143 standard; protein; 748 AA.
AC   W50143;
DT   28-AUG-1998  (first entry)
DE   Cyanobacterial phytochrome Cph1 apoprotein.
KW   Phytofluor; fluorescent label; phytochrome; Cph1; cyanobacterium.
OS   Synechocystis sp. strain PCC6803.
FH   Key             Location/Qualifiers
FT   Modified_site   538
FT                   /note= "undetermined amino acid residue"
FT   Peptide         536..544
FT                   /note= "histidine kinase transmitter module
FT                         conserved motif"
FT   Peptide         642..653
FT                   /note= "histidine kinase transmitter module
FT                         conserved motif"
FT   Peptide         679..687
FT                   /note= "histidine kinase transmitter module
FT                         conserved motif"
FT   Peptide         694..698
FT                   /note= "histidine kinase transmitter module
FT                         conserved motif"
FT   Peptide         709..714
FT                   /note= "histidine kinase transmitter module
FT                         conserved motif"
PN   WO9805944-A1.
PD   12-FEB-1998.
PF   01-AUG-1997; U13529.
PR   02-AUG-1996; US-023217.
PA   (REGC ) UNIV CALIFORNIA.
PI   Lagarias JC, Murphy JT;
DR   WPI; 98-145711/13.
PT   Adducts of apoprotein polypeptide and chromophore as label,
PT   particularly for bio-molecules - used as fluorescent markers in
PT   immunoassays, nucleic acid hybridisation, detecting protein-protein
PT   interaction etc., are stable with high molar absorption
PS   Example 4; Fig 10B; 87pp; English.
CC   This polypeptide comprises cyanobacterial phytochrome 1 (Cph1) of
CC   Synechocystis sp. PCC6803.  Its amino acid sequence was deduced
CC   from locus slr0473 genomic DNA.  Expression of the 748-residue
CC   polypeptide in E. coli and incubation with phycocyanobilin yields
CC   an adduct with a red, far-red photoreversible phytochrome
CC   signature.  The invention provides a new class of fluorescent
CC   protein adducts (designated phytofluors) that are generally suitable
CC   for use as fluorescent markers.  They comprise a protein component
CC   (an apoprotein) and a bilin chromophore such as phycoerythrobilin.
CC   Preferred apoproteins are obtained from plants, e.g. oats (see
CC   W50144), from green algae, e.g. Mesotaenium caldariorum (see
CC   W50145), or cyanobacteria such as Synechocystis.  Truncated
CC   apoproteins consisting of the N-terminal chromophore domain are
CC   especially preferred.  Recombinant apoproteins assemble
CC   spontaneously with the bilin chromophore.  Claimed compositions
CC   comprise a protein, glycoprotein, antibody or nucleic acid to be
CC   detected linked to the fluorescent adduct.  They are used in assays
CC   for detecting the other member of a specific binding pair, e.g.
CC   immunoassay of antigens, immuno-histochemical labelling, as nucleic
CC   acid probes for Southern blotting, for identification of manufactured
CC   products, also to detect protein-protein interactions, including
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CC   studies on intracellular protein localisation and identification of
CC   transfected cells.  The phytofluors make ideal fluorescent markers
CC   because they have a long wavelength absorption maximum and high
CC   molar absorption coefficient, and are stable to light and pH.
SQ   Sequence   748 AA;

  Query Match           27.6%;  Score 403;  DB 32;  Length 748;
  Best Local Similarity  36.5%;  Pred. No. 1.50e-27;
  Matches   62;  Conservative   51;  Mismatches  49;  Indels   8;  Gaps   8;

Db    139 manaalnrlrq-qa-nlrdfydviveevrrmlqfqrvmlyrrdennhcdvialdkrddme 196
          :|  |::||:   : ::  : | :||:|:|:  ::|||:|:  |::| :|::  :| |:|
Qy      2 LAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDLE 61

Db    197 pllqlhypesdipqparrifihnpirvipdvygvavpltpavnpstnravdltesilrsa 256
          | | |||| :||||:|| :| :| :|:| |  : :| :  : :   :|:: | :| ||::
Qy     62 PYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQS-E-ELKRPLCLVNSTLRAP 119

Db    257 yhchltylknmg-vga-sttisli-kdg-hlwgliachhqtpkvipnelr 302
            ||  |: ||| |:: : :| :  ||:  ||||:  || :|: :|  ||
Qy    120 HGCHTQYMANMGSVASLALAIVVKGKDSSKLWGLVVGHHCSPRYVPFPLR 169


RESULT    4
ID   P70204 standard; protein; 353 AA.
AC   P70204;
DT   09-APR-1991  (first entry)
DE   Sequence of human inhibin beta-chain precursor beta-B
KW   Fertility control; contraception; hormone; spermatogenesis.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   modified_site   38..40
FT                   /note="potential N-linked glycosylation sites"
FT   region          1..237
FT                   /note="used to design a long synthetic DNA probe"
FT   protein         238..343
FT   cleavage_site   235..237
FT                   /note="proteolytic processing site"
PN   EP-222491-A.
PD   20-MAY-1987.
PF   02-OCT-1986; 307586.
PR   03-OCT-1985; US-783910.
PR   10-FEB-1986; US-827710.
PR   12-SEP-1986; US-906729.
PA   (GETH ) GENENTECH INC.
PI   Mason AJ, Seeburg PH;.
DR   WPI; 87-137512/20.
DR   N-PSDB; N70316.
PT   Recombinant human or porcine inhibin or activin - used for
PT   modulating clinical condition or reproductive physiology of
PT   animals.
PS   Disclosure; Fig 9A; 48pp; English.
CC   A compsn. comprising human or porcine inhibin which is completely
CC   free of unidentified or porcine proteins is claimed.  Also claimed
CC   are non chromosomal DNA encoding inhibin-alpha or an inhibin-beta
CC   chain.  Sequencing of inhibin-encoding cDNA has led to the
CC   identification of prodomain regions located N-terminal to the
CC   mature inhibin chains that represent coordinately expressed
CC   biologically active polypeptides.  The prodomain regions or
CC   prodomain immunogens are useful in monitoring preproinhibin
CC   processing in transformant cell culture or in experiments directed
CC   at modulating the clinical condt. or reproductive physiology of
CC   animals.
SQ   Sequence   353 AA;

  Query Match            7.1%;  Score 104;  DB 2;  Length 353;
  Best Local Similarity  35.2%;  Pred. No. 2.65e+00;
  Matches   31;  Conservative   19;  Mismatches  27;  Indels  11;  Gaps  11;

Db    144 rvkvy-fqeqghgdrwnmvekrvdlkrs-gwhtfplteaiqal-fergerrlnldvqcds 200
          ||:|| |:|: ||:  : : :| ||    | | :| |:  ||  |   : |: : : ||
Qy     37 RVMVYQFHEDDHGEVVSEI-RRSDLEPYLGLH-YPATDIPQAARFLFKQNRVRM-I-CD- 91

Db    201 cqelavvpvfvdpgeeshrpfvvvqarl 228
          |   : |:| |:: ||  ||: :| : |
Qy     92 CNA-TPVKV-VQS-EELKRPLCLVNSTL 116


RESULT    5
ID   P70852 standard; protein; 91 AA.
AC   P70852;
DT   09-APR-1991  (first entry)
DE   Sequence of inhibin beta-B chain prodomain
KW   Fertility control; contraception; hormone; spermatogenesis.
PN   EP-222491-A.
PD   20-MAY-1987.
PF   02-OCT-1986; 307586.
PR   03-OCT-1985; US-783910.
PR   10-FEB-1986; US-827710.
PR   12-SEP-1986; US-906729.
PA   (GETH ) GENENTECH INC.
PI   Mason AJ, Seeburg PH;.
DR   WPI; 87-137512/20.
PT   Recombinant human or porcine inhibin or activin - used for
PT   modulating clinical condition or reproductive physiology of
PT   animals.
PS   Claim 30(b); p 22; 48pp; English.
CC   A compsn. comprising human or porcine inhibin which is completely
CC   free of unidentified or porcine proteins is claimed.  Also claimed
CC   are non chromosomal DNA encoding inhibin-alpha or an inhibin-beta
CC   chain.  Sequencing of inhibin-encoding cDNA has led to the
CC   identification of prodomain regions located N-terminal to the
CC   mature inhibin chains that represent coordinately expressed
CC   biologically active polypeptides.  The prodomain regions or
CC   prodomain immunogens are useful in monitoring preproinhibin
CC   processing in transformant cell culture or in experiments directed
CC   at modulating the clinical condt. or reproductive physiology of
CC   animals.
SQ   Sequence   91 AA;

  Query Match            6.9%;  Score 101;  DB 2;  Length 91;
  Best Local Similarity  34.9%;  Pred. No. 4.51e+00;
  Matches   30;  Conservative   18;  Mismatches  29;  Indels   9;  Gaps   9;

Db      2 rvkvy-fqeqghgdrwnmvekrvdlkrs-gwhtfplteaiqal-fergelnlsvqcdscq 58
          ||:|| |:|: ||:  : : :| ||    | | :| |:  ||  |   :  : : || |
Qy     37 RVMVYQFHEDDHGEVVSEI-RRSDLEPYLGLH-YPATDIPQAARFLFKQNRVRMICD-CN 93

Db     59 elavvpvfvdpgeeshrpfvvvqarl 84
          : | | |:: ||  ||: :| : |
Qy     94 A-TPVKV-VQS-EELKRPLCLVNSTL 116


RESULT    6
ID   W73007 standard; Protein; 621 AA.
AC   W73007;
DT   02-FEB-1999  (first entry)
DE   Cobra venom protease mocarhagin NMM-1.
KW   Mocarhagin; snake venom; Mozambiquan spitting cobra; protease;
KW   inflammation; myocardial infarction; thrombosis; infection;
KW   metastasis; therapy; NMM-1.
OS   Naja mossambica mossambica.
FH   Key             Location/Qualifiers
FT   Peptide         1..23
FT                   /label= Sig_peptide
FT   Protein         24..621
FT                   /label= Mat_protein
PN   WO9846771-A2.
PD   22-OCT-1998.
PF   14-APR-1998; U07998.
PR   18-FEB-1998; US-026001.
PR   15-APR-1997; US-843373.
PR   23-JAN-1998; US-012637.
PA   (GEMY ) GENETICS INST INC.
PI   Boodhoo A, Sako D, Seehra JS, Shaw G;
DR   WPI; 98-568735/48.
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DR   N-PSDB; V07895.
PT   Isolated mocarhagin cobra venom protease, and nucleic acids encoding
PT   it - used to develop products for treating e.g. myocardial
PT   infarction, thrombosis, bacterial or viral infection, metastatic
PT   conditions or inflammatory disorders
PS   Claim 21; Page 35-38; 97pp; English.
CC   This is the amino acid sequence of mocarhagin NMM-1, a highly
CC   specific metalloproteinase from the venom of the Mozambiquan
CC   spitting cobra.  The invention provides mocarhagin polypeptides
CC   (see W73007-13) and polynucleotides (see V07895-901) encoding them,
CC   as well as host cells and methods of producing the (especially
CC   mature) polypeptides.  Mocarhagin proteins are capable of cleaving
CC   anionic polypeptide containing sulphated tyrosine residues,
CC   P-selectin glycoprotein (GP) ligand-1 (PSGL-1) and GP1b-alpha
CC   (claimed).  They also inhibit neutrophil/HL60 binding, inhibit
CC   platelet binding to von Willebrand Factor, require Ca2+ and Zn2+
CC   ions for activity and have activity inhibited by excess EDTA or
CC   high concentrations of DFP (claimed).  They can be used to inhibit
CC   selectin-mediated binding and to treat inflammatory disease
CC   (claimed).  In particular, they can be used to treat e.g. myocardial
CC   infarction, vessel restenosis, thrombosis, bacterial or viral
CC   infection, metastatic conditions, inflammatory disorders such as
CC   arthritis, acute respiratory distress syndrome, asthma, emphysema,
CC   delayed type hypersensitivity reaction, systemic lupus
CC   erythematosus, thermal injury such as burns or frostbite,
CC   autoimmune thyroiditis, experimental allergic encephalomyelitis,
CC   multiple sclerosis, multiple organ injury syndrome secondary to
CC   trauma, diabetes, Reynaud's syndrome, neutrophilic dermatosis
CC   (Sweet's syndrome), inflammatory bowel disease, Grave's disease,
CC   glomerulonephritis, gingivitis, periodontitis, haemolytic uremic
CC   syndrome, ulcerative colitis, Crohn's disease, necrotising
CC   enterocolitis, granulocyte transfusion associated syndrome,
CC   cytokine-induced enterocolitis, granulocyte transfusion associated
CC   syndrome, or cytokine-induced toxicity.  Mocarhagin protein may
CC   also be useful in organ transplantation, both to prepare organs for
CC   transplantation and to quell organ transplant rejection, to treat
CC   haemodialysis and leukophoresis patients, or as an inhibitor of P-
CC   or E-selectin-mediated intercellular adhesion.
SQ   Sequence   621 AA;

  Query Match             6.4%;  Score 94;  DB 37;  Length 621;
  Best Local Similarity  30.9%;  Pred. No. 1.53e+01;
  Matches    17;  Conservative    9;  Mismatches  27;  Indels   2;  Gaps   1;

Db     39 vpalskggvqnpqpetkyedtmqyefhvngepvvlhlernkglfsedytethyap 93
          : ||    |:: |  | |:  | |:|| :    |:   |   |  | |   ||::
Qy     18 IGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL--EPYLGLHYPA 70


RESULT    7
ID   P70201 standard; protein; 351 AA.
AC   P70201;
DT   09-APR-1991  (first entry)
DE   Sequence of porcine inhibin beta-chain precursor beta-B.
KW   Fertility control; contraception; hormone; spermatogenesis.
OS   Sus scrofa domestica.
FH   Key             Location/Qualifiers
FT   region          1..270
FT                   /note="used to design a long synthetic DNA probe"
FT   protein         271..386
FT   cleavage_site   268..270
FT                   /note="proteolytic processing site"
PN   EP-222491-A.
PD   20-MAY-1987.
PF   02-OCT-1986; 307586.
PR   03-OCT-1985; US-783910.
PR   10-FEB-1986; US-827710.
PR   12-SEP-1986; US-906729.
PA   (GETH ) GENENTECH INC.
PI   Mason AJ, Seeburg PH;.
DR   WPI; 87-137512/20.
DR   N-PSDB; N70318.
PT   Recombinant human or porcine inhibin or activin - used for
PT   modulating clinical condition or reproductive physiology of
PT   animals.
PS   Disclosure; Fig 2B; 48pp; English.
CC   A compsn. comprising human or porcine inhibin which is completely
CC   free of unidentified or porcine proteins is claimed.  Also claimed
CC   are non chromosomal DNA encoding inhibin-alpha or an inhibin-beta
CC   chain.  Sequencing of inhibin-encoding cDNA has led to the
CC   identification of prodomain regions located N-terminal to the
CC   mature inhibin chains that represent coordinately expressed
CC   biologically active polypeptides.  The prodomain regions or
CC   prodomain immunogens are useful in monitoring preproinhibin
CC   processing in transformant cell culture or in experiments directed
CC   at modulating the clinical condt. or reproductive physiology of
CC   animals.
SQ   Sequence   351 AA;

  Query Match             6.2%;  Score 91;  DB 2;  Length 351;
  Best Local Similarity  35.2%;  Pred. No. 2.57e+01;
  Matches    31;  Conservative   16;  Mismatches  30;  Indels  11;  Gaps  11;

Db    140 rvkvy-fqepghgdrwdvvekrvdlkrs-gwhtlplteaiqal-fergerrlnldvqcdg 196
          ||:|| |:|  ||:    : :| ||    | |  | |:  ||  |   : |: : : ||
Qy     37 RVMVYQFHEDDHGEVVSEI-RRSDLEPYLGLH-YPATDIPQAARFLFKQNRVRM-I-CD- 91

Db    197 cqelavvpvfvdpgeeshrpfvvvqarl 224
          |   : | | |:: ||  ||: :| : |
Qy     92 CNA-TPVKV-VQS-EELKRPLCLVNSTL 116


RESULT    8
ID   W73009 standard; Protein; 613 AA.
AC   W73009;
DT   02-FEB-1999  (first entry)
DE   Cobra venom protease mocarhagin NMM-9.
KW   Mocarhagin; snake venom; Mozambiquan spitting cobra; protease;
KW   inflammation; myocardial infarction; thrombosis; infection;
KW   metastasis; therapy; NMM-9.
OS   Naja mossambica mossambica.
FH   Key             Location/Qualifiers
FT   Peptide         1..23
FT                   /label= Sig_peptide
FT   Protein         24..613
FT                   /label= Mat_protein
PN   WO9846771-A2.
PD   22-OCT-1998.
PF   14-APR-1998; U07998.
PR   18-FEB-1998; US-026001.
PR   15-APR-1997; US-843373.
PR   23-JAN-1998; US-012637.
PA   (GEMY ) GENETICS INST INC.
PI   Boodhoo A, Sako D, Seehra JS, Shaw G;
DR   WPI; 98-568735/48.
DR   N-PSDB; V07897.
PT   Isolated mocarhagin cobra venom protease, and nucleic acids encoding
PT   it - used to develop products for treating e.g. myocardial
PT   infarction, thrombosis, bacterial or viral infection, metastatic
PT   conditions or inflammatory disorders
PS   Claim 40; Page 45-48; 97pp; English.
CC   This is the amino acid sequence of mocarhagin NMM-9, a highly
CC   specific metalloproteinase from the venom of the Mozambiquan
CC   spitting cobra.  The invention provides mocarhagin polypeptides
CC   (see W73007-13) and polynucleotides (see V07895-901) encoding them,
CC   as well as host cells and methods of producing the (especially
CC   mature) polypeptides.  Mocarhagin proteins are capable of cleaving
CC   anionic polypeptide containing sulphated tyrosine residues,
CC   P-selectin glycoprotein (GP) ligand-1 (PSGL-1) and GP1b-alpha
CC   (claimed).  They also inhibit neutrophil/HL60 binding, inhibit
CC   platelet binding to von Willebrand Factor, require Ca2+ and Zn2+
CC   ions for activity and have activity inhibited by excess EDTA or
CC   high concentrations of DFP (claimed).  They can be used to inhibit
CC   selectin-mediated binding and to treat inflammatory disease
CC   (claimed).  In particular, they can be used to treat e.g. myocardial
CC   infarction, vessel restenosis, thrombosis, bacterial or viral
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CC   infection, metastatic conditions, inflammatory disorders such as
CC   arthritis, acute respiratory distress syndrome, asthma, emphysema,
CC   delayed type hypersensitivity reaction, systemic lupus
CC   erythematosus, thermal injury such as burns or frostbite,
CC   autoimmune thyroiditis, experimental allergic encephalomyelitis,
CC   multiple sclerosis, multiple organ injury syndrome secondary to
CC   trauma, diabetes, Reynaud's syndrome, neutrophilic dermatosis
CC   (Sweet's syndrome), inflammatory bowel disease, Grave's disease,
CC   glomerulonephritis, gingivitis, periodontitis, haemolytic uremic
CC   syndrome, ulcerative colitis, Crohn's disease, necrotising
CC   enterocolitis, granulocyte transfusion associated syndrome,
CC   cytokine-induced enterocolitis, granulocyte transfusion associated
CC   syndrome, or cytokine-induced toxicity.  Mocarhagin protein may
CC   also be useful in organ transplantation, both to prepare organs for
CC   transplantation and to quell organ transplant rejection, to treat
CC   haemodialysis and leukophoresis patients, or as an inhibitor of P-
CC   or E-selectin-mediated intercellular adhesion.
SQ   Sequence   613 AA;

  Query Match             6.2%;  Score 90;  DB 37;  Length 613;
  Best Local Similarity  29.1%;  Pred. No. 3.04e+01;
  Matches    16;  Conservative   10;  Mismatches  27;  Indels   2;  Gaps   1;

Db     39 vpalskggvqnpqpetkyedtmqyefqvngepvvlhlernkglfsedytethyas 93
          : ||    |:: |  | |:  | |:|: :    |:   |   |  | |   ||::
Qy     18 IGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL--EPYLGLHYPA 70


RESULT    9
ID   W73013 standard; Protein; 621 AA.
AC   W73013;
DT*  02-FEB-1999  (first entry)
DE   Cobra venom mocarhagin NMM-9ek.
KW   Mocarhagin; snake venom; Mozambiquan spitting cobra; protease;
KW   inflammation; myocardial infarction; thrombosis; infection;
KW   metastasis; therapy; NMM-9ek.
OS*  Naja mossambica mossambica.
OS   Synthetic.
FH   Key             Location/Qualifiers
FT   Peptide         1..196
FT                   /label= Pro_peptide
FT   Cleavage_site   192..196
FT                   /note= "enterokinase cleavage site"
FT   Protein         197..621
FT                   /label= Mat_protein
PN   WO9846771-A2.
PD   22-OCT-1998.
PF   14-APR-1998; U07998.
PR   18-FEB-1998; US-026001.
PR   15-APR-1997; US-843373.
PR   23-JAN-1998; US-012637.
PA   (GEMY ) GENETICS INST INC.
PI   Boodhoo A, Sako D, Seehra JS, Shaw G;
DR   WPI; 98-568735/48.
DR   N-PSDB; V07901.
PT   Isolated mocarhagin cobra venom protease, and nucleic acids encoding
PT   it - used to develop products for treating e.g. myocardial
PT   infarction, thrombosis, bacterial or viral infection, metastatic
PT   conditions or inflammatory disorders
PS   Claim 80; Page 65-68; 97pp; English.
CC   This is the amino acid sequence of a modified cobra venom mocarhagin
CC   protein, termed NMM-9ek, that includes an enterokinase cleavage site
CC   between the propeptide and mature peptide of mocarhagin (see also
CC   W73009).  Introduction of the cleavage site may allow secretion of
CC   active mocarhagin from eukaryotic host cells.  The invention
CC   provides mocarhagin polypeptides (see W73007-13) and polynucleotides
CC   (see V07895-901), as well as host cells and methods of producing
CC   (especially mature) polypeptides.  Mocarhagin proteins are capable
CC   of cleaving anionic polypeptide containing sulphated tyrosine
CC   residues, P-selectin glycoprotein (GP) ligand-1 (PSGL-1) and
CC   GP1b-alpha (claimed).  They also inhibit neutrophil/HL60 binding,
CC   inhibit platelet binding to von Willebrand Factor, require Ca2+ and
CC   Zn2+ ions for activity and have activity inhibited by excess EDTA
CC   or high concentrations of DFP (claimed).  They can be used for
CC   inhibiting selectin-mediated binding and for treating an
CC   inflammatory disease (claimed).  In particular, they can be used
CC   for treating e.g. myocardial infarction, vessel restenosis,
CC   thrombosis, bacterial or viral infection, metastatic conditions,
CC   inflammatory disorders such as arthritis, acute respiratory distress
CC   syndrome, asthma, emphysema, delayed type hypersensitivity reaction,
CC   systemic lupus erythematosus, thermal injury e.g. burns or frostbite,
CC   autoimmune thyroiditis, experimental allergic encephalomyelitis,
CC   multiple sclerosis, multiple organ injury syndrome secondary to
CC   trauma, diabetes, Reynaud's syndrome, neutrophilic dermatosis
CC   (Sweet's syndrome), inflammatory bowel disease, Grave's disease,
CC   glomerulonephritis, gingivitis, periodontitis, haemolytic uremic
CC   syndrome, ulcerative colitis, Crohn's disease, necrotising
CC   enterocolitis, granulocyte transfusion associated syndrome,
CC   cytokine-induced enterocolitis, granulocyte transfusion associated
CC   syndrome, or cytokine-induced toxicity.  Mocarhagin protein may
CC   also be useful in organ transplantation, both to prepare organs for
CC   transplantation and to quell organ transplant rejection, to treat
CC   haemodialysis and leukophoresis patients, or as an inhibitor of P-
CC   or E-selectin-mediated intercellular adhesion.
SQ   Sequence   621 AA;

  Query Match             6.2%;  Score 90;  DB 37;  Length 621;
  Best Local Similarity  29.1%;  Pred. No. 3.04e+01;
  Matches    16;  Conservative   10;  Mismatches  27;  Indels   2;  Gaps   1;

Db     39 vpalskggvqnpqpetkyedtmqyefqvngepvvlhlernkglfsedytethyas 93
          : ||    |:: |  | |:  | |:|: :    |:   |   |  | |   ||::
Qy     18 IGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL--EPYLGLHYPA 70


RESULT   10
ID   P81326 standard; protein; 638 AA.
AC   P81326;
DT   23-OCT-1990  (first entry)
DE   Human growth hormone receptor.
KW   Growth hormone receptor; gigantism; acromegaly.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   peptide         1..18
FT                   /label=signal_sequence
PN   WO8809818-A.
PD   15-DEC-1988.
PF   10-JUN-1988; U02008.
PR   12-JUN-1987; US-062542.
PA   (GETH) Genentech Inc.
PI   Hammonds RG, Leungh DW, Spencer SA, Wood WI;
DR   WPI; 88-368632/51.
DR   N-PSDB; N81716.
PT   New pure growth hormone receptor and binding protein - for treating
PT   growth hormone abnormalities, and new encoding DNA sequences.
PS   Disclosure; 1pp; English.
CC   The sequence was deduced from a clone isolated from an adult liver
CC   cDNA lambda gt10 library.   The DNA can be inserted into an
CC   expression vector for prodn. of the recombinant GHR which is used
CC   to treat GH-related disorders such as gigantism and acromegaly.
CC   A hydropathy plot revealed an extracellular GH binding domain, a
CC   transmembrane domain, and an intracellular signalling domain.  Eight
CC   potential N-linked glycosylation sites are predicted.
CC   See also P81327 and N81718-9.
SQ   Sequence   638 AA;

  Query Match             6.1%;  Score 89;  DB 1;  Length 638;
  Best Local Similarity  27.3%;  Pred. No. 3.60e+01;
  Matches    18;  Conservative   17;  Mismatches  27;  Indels   4;  Gaps   4;

Db    285 flfskqqrikmlslppvpvpkikgidpdllkegkleevntilaihdsykpefhsddswve 344
          ||| || |::|:     : | :| :::: ||   |  ||: |    :   :: :: : |
Qy     79 FLF-KQNRVRMIC-DCNATP-VKVVQSEELKRP-LCLVNSTLRAPHGCHTQYMANMGSVA 134

Db    345 fieldi 350
           : | |
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Qy    135 SLALAI 140


RESULT   11
ID   W28089 standard; Protein; 236 AA.
AC   W28089;
DT   01-SEP-1998  (first entry)
DE   Amino acid sequence of DNA repair protein RECN (recombination protein N).
KW   Staphylococcus aureus protein; ribozyme; antisense sequence; control;
KW   Staphylococcal gene; regulatory element; bacterial gene expression;
KW   vaccine; Staphylococcal infection; food poisoning; scaled skin syndrome;
KW   toxic shock syndrome.
OS   Staphylococcus aureus.
FH   Key             Location/Qualifiers
FT   Misc_difference 1..236
FT                   /note= "residues designated X are not defined in
FT                         the specification"
PN   WO9730070-A1.
PD   21-AUG-1997.
PF   19-FEB-1997; U02318.
PR   20-FEB-1996; US-011888.
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PI   Black MT, Burnham MK, Hodgson JE, Knowles DJC, Nicholas RO,
PI   Pratt JM, Reichard RW, Rosenberg M, Ward JM;
DR   WPI; 97-424969/39.
DR   N-PSDB; T84026.
PT   Novel polypeptide(s) from Staphylococcus aureus strain WCUH29 - used
PT   to isolate antimicrobial compounds, and in vaccines against S.
PT   aureus infection
PS   Claim 6; Page 458; 989pp; English.
CC   The present sequence represents a Staphylococcus aureus protein, that,
CC   based on homology with a Bacillus subtilis protein, is believed to be a
CC   DNA repair protein RECN (recombination protein N). The DNA sequence was
CC   isolated from a library of clones of S. aureus WCUH 29 in Escherichia
CC   coli. The DNA sequence can be used in the construction of ribozymes and
CC   antisense sequences to control the expression of Staphylococcal genes.
CC   The DNA sequence is also useful as a source of regulatory elements for
CC   the control of bacterial gene expression. The present protein may be used
CC   to produce vaccines to enable a host to produce specific antibodies
CC   with antibacterial action. These vaccines and antibodies would protect
CC   a host against invasion by S. aureus, and conditions relating to
CC   Staphylococcal infection, e.g. Staphylococcal food poisoning, scaled
CC   skin syndrome, and toxic shock syndrome.
SQ   Sequence   236 AA;

  Query Match           6.0%;  Score 87;  DB 31;  Length 236;
  Best Local Similarity  23.9%;  Pred. No. 5.05e+01;
  Matches   17;  Conservative   22;  Mismatches  30;  Indels   2;  Gaps   2;

Db    159 einalynqvievgqalskqrrivarelrdhivseiqnlqmkdanleisfkkleepnidgi 218
          :| || : |:|  | |:   |::  ::::   :|: : ::: ::|| ::  |  |  |
Qy     17 DIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVS-EIRRSDLE-PYLGLHYPATDIP 74

Db    219 efveflxtpnk 229
          :   ||   |:
Qy     75 QAARFLFKQNR 85


RESULT   12
ID   W03178 standard; Protein; 746 AA.
AC   W03178;
DT   24-FEB-1997  (first entry)
DE   Human poly-immunoglobulin receptor.
KW   Human; immunoglobulin; receptor; protection protein; mutans;
KW   heavy chain; antigen binding domain; protection; pathogen;
KW   mucosal; environment; gastrointestinal; passive; immunisation;
KW   Guy's 13 antibody; prevention; dental caries; Streptococcus;
KW   poly; sorbinus.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   region          13..45
FT                   /note= "putative immunoglobulin binding residues
FT                   of domain I"
FT   domain          1..120
FT                   /label= domain_I
FT   domain          110..230
FT                   /label= domain_II
FT   domain          210..340
FT                   /label= domain_III
FT   domain          320..450
FT                   /label= domain_IV
FT   domain          440..550
FT                   /label= domain_V
FT   region          550..606
FT                   /note= "external portions of domain VI"
FT   region          550..627
FT                   /note= "external portions of domain VI"
FT   region          625..660
FT                   /label= transmembrane_segment
FT   region          650..746
FT                   /label= intracellular_portion
PN   WO9621012-A1.
PD   11-JUL-1996.
PF   27-DEC-1995; U16889.
PR   30-DEC-1994; US-367395.
PR   04-MAY-1995; US-434000.
PA   (PLAN-) PLANT BIOTECHNOLOGY INC.
PA   (UNME-) UNITED MEDICAL & DENTAL SCHOOLS GUYS.
PA   (PLAN-) PLANET BIOTECHNOLOGY INC.
PI   Hiatt AC,  Lehner T,  Ma JKC;
DR   WPI; 96-333987/33.
DR   N-PSDB; T31288.
PT   Immunoglobulin and protection protein complex and its prodn. in
PT   plants - useful for passive immunisation against mucosal antigens,
PT   esp. against S. mutans and S. sorbinus to prevent dental caries
PS   Disclosure; Pages 105-108; 152pp; English.
CC   The present sequence is the human poly-immunoglobulin (Ig)
CC   receptor, a portion of which corresp. to residues 1-627, pref.
CC   1-606, or esp. residues 13-45, 1-120, 110-230, 210-340, 320-450,
CC   440-550, 550-606 or 550-627 comprises a protection protein (PP).
CC   The Ig of the invention comprises a PP as above in association with
CC   an Ig derived heavy chain, having at least a portion of an antigen
CC   (Ag) binding domain. The PP protects the Ig in harsh mucosal, e.g.
CC   gastrointestinal, environments, therefore enhancing its
CC   effectiveness in passively immunising animals against mucosal
CC   pathogens. The Ag binding domain is specifically derived from the
CC   Guy's 13 antibody, and the Ig can be used to prevent dental caries
CC   by binding, e.g. Streptococcus mutans serotypes c, e and f, or
CC   S. sorbinus serotypes d and g.
SQ   Sequence   746 AA;

  Query Match           6.0%;  Score 87;  DB 20;  Length 746;
  Best Local Similarity  28.3%;  Pred. No. 5.05e+01;
  Matches   15;  Conservative   14;  Mismatches  20;  Indels   4;  Gaps   4;

Db    258 gencdvvvntlgkrapafegrillnpqdkdgsfsvvitglrkedagrylcgah 310
          |  || ||: :  |  ::: |:::  |  :   : |:: :|: |   || | |
Qy     19 GALCDTVVEDV-QRLTGYD-RVMVY-QFHEDDHGEVVSEIRRSDLEPYL-GLH 67


RESULT   13
ID   P95645 standard; protein; 1873 AA.
AC   P95645;
DT   21-MAR-1990  (first entry)
DE   Rabbit seletal muscle alpha-1 sub-unit gene product.
KW   Skeletal muscle
OS   Sylvilagus (rabbit).
PN   WO8909834-A.
PD   19-OCT-1989.
PF   04-APR-1988; 001408.
PR   04-APR-1988; US-176899.
PA   (SALK) Salk Inst for Biol Stud.
PI   Ellis SB, Williams ME, Harpold MM, Schwartz A, Sartor J;
DR   WPI; 89-324236/44.
DR   N-PSDB; N91778.
PT   New DNA encoding alpha-2 subunit of animal calcium channel - also new
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product and eukaryotic cells for testing cpds. for calcium
st or antagonist activity
closure; page 16-1 to 18-3; 68pp; English.
also used to diagnose Lambert-Eaton syndrome by reacting test serum
CC with alpha-1 and alpha-2 subunits. Labelled fragments can be used as
CC probes.
SQ Sequence 1873 AA;

Query Match 6.0%; Score 87; DB 1; Length 1873;
Best Local Similarity 35.4%; Pred. No. 5.05e+01;
Matches 17; Conservative 8; Mismatches 20; Indels 3; Gaps 3;

Db 746 eedepeipvsprprplae-lqlkekavpipeasssfifsptnkvrvlc 792
|:| |: | | | | | ||:|: |:| |:||::|
Qy 45 EDDHGEVVSEIRRSDLEPYLGLHYPATDIPQAAR-FLFKQ-NRVRMIC 90

RESULT 14
ID W18390 standard; Protein; 1873 AA.
AC W18390;
DT 05-AUG-1997 (first entry)
DE Rabbit calcium channel alpha-1 subunit.
KW Rabbit; skeletal muscle; calcium channel; alpha-2; subunit; alpha-1;
KW transformation; reporter gene; screening assay; agonist; antagonist.
OS Oryctolagus cuniculus.
FH Key Location/Qualifiers
FT region 52..70
FT /note= "Transmembrane region"
FT modified_site 79
FT /note= "N-linked glycosylation site"
FT region 89..108
FT /note= "Transmembrane region"
FT region 121..139
FT /note= "Transmembrane region"
FT region 161..179
FT /note= "Transmembrane region"
FT region 199..218
FT /note= "Transmembrane region"
FT modified_site 257
FT /note= "N-linked glycosylation site"
FT region 310..334
FT /note= "Transmembrane region"
FT region 433..451
FT /note= "Transmembrane region"
FT region 467..486
FT /note= "Transmembrane region"
FT region 495..513
FT /note= "Transmembrane region"
FT region 524..542
FT /note= "Transmembrane region"
FT region 562..581
FT /note= "Transmembrane region"
FT region 637..661
FT /note= "Transmembrane region"
FT modified_site 687
FT /note= "Potential cAMP-dependent phosphorylation site"
FT modified_site 797
FT /note= "N-linked glycosylation site"
FT region 800..818
FT /note= "Transmembrane region"
FT region 835..854
FT /note= "Transmembrane region"
FT region 967..885
FT /note= "Transmembrane region"
FT region 893..912
FT /note= "Transmembrane region"
FT region 931..950
FT /note= "Transmembrane region"
FT region 1041..1065
FT /note= "Transmembrane region"
FT region 1119..1137
FT /note= "Transmembrane region"
FT region 1153..1172
FT /note= "Transmembrane region"
FT region 1181..1199
FT /note= "Transmembrane region"
FT region 1232..1250
FT /note= "Transmembrane region"
FT region 1270..1289
FT /note= "Transmembrane region"
FT region 1357..1381
FT /note= "Transmembrane region"
FT modified_site 1464
FT /note= "N-linked glycosylation site"
FT modified_site 1502
FT /note= "Potential cAMP-dependent phosphorylation site"
FT modified_site 1552
FT /note= "Potential cAMP-dependent phosphorylation site"
FT modified_site 1575
FT /note= "Potential cAMP-dependent phosphorylation site"
FT modified_site 1674
FT /note= "N-linked glycosylation site"
FT modified_site 1757
FT /note= "Potential cAMP-dependent phosphorylation site"
FT modified_site 1772
FT /note= "Potential cAMP-dependent phosphorylation site"
FT modified_site 1854
FT /note= "Potential cAMP-dependent phosphorylation site"
PN US5618720-A.
PD 08-APR-1997.
PF 04-APR-1988; 176899.
PR 04-APR-1988; US-176899.
PR 04-APR-1989; WO-U01408.
PR 04-APR-1989; US-603751.
PR 13-JUL-1992; US-914231.
PR 28-SEP-1994; US-314083.
PR 15-FEB-1995; US-404354.
PA (SIBI-) SIBIA NEUROSCIENCES INC.
PI Brenner R, Ellis SB, Harpold MM, Sartor J, Schwartz A;
PI Williams ME;
DR WPI; 97-225431/20.
DR N-PSDB; T70228.
PT Eukaryotic cell expressing heterologous calcium channel - comprising
PT alpha-1 and alpha-2 sub:units; used in drug screening assays
PS Claim 3; Column 17-30; 50pp; English.
CC This sequence represents the rabbit skeletal muscle calcium channel
CC alpha-1 subunit. This protein comprises twenty-four potential
CC transmembrane regions and has a molecular weight of 212143. The
CC protein contains four internal repeated segments. Each repeat
CC comprises five hydrophobic segments and one segment with strong
CC positive charge. The alpha-1 protein lacks a hydrophobic amino
CC terminal sequence characteristic of a signal peptide and it is
CC thought that the four internal repeats represent the 24 transmembrane
CC segments and that the N- and C-termini are extracellular. This
CC sequence may be used, in conjunction with the alpha-2 subunit coding
CC sequence (see also T70227) to transform a eukaryotic cell. The cell
CC may be used optionally with a reporter gene, in screening assays for
CC Ca2+ channel agonists or antagonists.
SQ Sequence 1873 AA;

Query Match 6.0%; Score 87; DB 22; Length 1873;
Best Local Similarity 35.4%; Pred. No. 5.05e+01;
Matches 17; Conservative 8; Mismatches 20; Indels 3; Gaps 3;

Db 746 eedepeipvsprprplae-lqlkekavpipeassffifsptnkvrvlc 792
|:| |: | | | | | ||:|: | :| |:||::|
Qy 45 EDDHGEVVSEIRRSDLEPYLGLHYPATDIPQAARF-LFKQ-NRVRMIC 90

RESULT 15
ID W37711 standard; Protein; 1873 AA.
AC W37711;
DT 10-MAR-1998 (first entry)
DE Rabbit skeletal calcium channel alpha-1 subunit.
KW Rabbit; skeletal; calcium channel alpha-1 subunit; hybridisation;
KW probe.

OS Oryctolagus cuniculus.
PN US5686241-A.
PD 11-NOV-1997.
PF 28-SEP-1994; 314083.
PR 08-NOV-1990; US-603751.
PR 04-APR-1988; US-176899.
PR 04-APR-1989; WO-U01408.
PR 13-JUL-1992; US-914231.
PR 28-SEP-1994; US-314083.
PA (SIBI-) SIBIA NEUROSCIENCES INC.
PI Brenner R, Ellis SB, Harpold MM, Schwartz A, Williams ME;
DR WPI; 97-558134/51.
DR N-PSDB; T96811.
PT Oligonucleotide probes - for identifying calcium channel alpha-2
PT subunits
PS Disclosure; Fig 1A-J; 44pp; English.
CC This is a rabbit skeletal muscle calcium channel alpha-1 subunit.
CC The DNA sequences of the alpha-2 subunit (rabbit and human -
CC see T96812-13) are useful as hybridisation probes for identifying nucleic
CC acids encoding all or part of a calcium channel alpha-2 subunit. Certain
CC diseases, e.g. Lambert-Eaton Syndrome, involve autoimmune interactions
CC with calcium channels. The ready availability of calcium channel subunits
CC would make possible immunoassays for diagnosis of such diseases and an
CC understanding of them at the molecular level that could lead to effective
CC methods for treating them.
SQ Sequence 1873 AA;

Query Match 6.0%; Score 87; DB 26; Length 1873;
Best Local Similarity 35.4%; Pred. No. 5.05e+01;
Matches 17; Conservative 8; Mismatches 20; Indels 3; Gaps 3;

```
Db   746 eedepeipvsprprplae-lqlkekavpipeassffifsptnkvrvlc 792
         |:|  |:    |   |   | |   |  ||:|: | :|   |:||::|
Qy    45 EDDHGEVVSEIRRSDLEPYLGLHYPATDIPQAARF-LFKQ-NRVRMIC 90
```

Search completed: Mon Sep 13 14:26:09 1999
Job time : 37 secs.

****

MPSRCH (TM)

****

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Sep 13 14:24:55 1999; MasPar time 10.30 Seconds
762.567 Million cell updates/sec

Tabular output not generated.

Title: >US-09-272-809-9
Description: (1-196) from US09272809.pep
Perfect Score: 1458
Sequence: 1 KLAVRAISRLQSLPGGDIGA.....QAFGLQLQMELQLASQLAEK 196

Scoring table: PAM 150
Gap 11

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir60
1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 44.061; Variance 81.846; scale 0.538

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1458	100.0	1112	2	S46313	phytochrome E - Arabi	9.32e-293
2	1143	78.4	1132	2	T03668	phytochrome B - commo	1.65e-221
3	1070	73.4	1172	1	FKMUB	phytochrome B - Arabi	4.30e-205
4	1066	73.1	1171	2	S14065	phytochrome B - rice	3.40e-204
5	1039	71.3	1164	2	B71429	phytochrome D - Arabi	3.90e-198
6	1030	70.6	577	2	S58130	phytochrome - moss (C	4.07e-196
7	1027	70.4	1129	2	S28431	phytochrome B - potat	1.92e-195
8	1019	69.9	1142	2	S62714	phytochrome 1b - Meso	1.19e-193
9	1016	69.7	1132	2	S37206	phytochrome - moss (P	5.60e-193
10	986	67.6	1303	2	S27396	phytochrome / protein	2.93e-186
11	969	66.5	1134	2	S31280	phytochrome - Martens	1.86e-182
12	963	66.0	210	2	S62721	phytochrome B2 - toma	4.09e-181
13	948	65.0	211	2	S62720	phytochrome B1 - toma	9.21e-178
14	931	63.9	1111	1	FKMUC	phytochrome C - Arabi	5.76e-174
15	886	60.8	1124	1	FKPUZ	phytochrome - zucchin	6.21e-164
16	883	60.6	1123	2	S20497	phytochrome A - potat	2.89e-163
17	865	59.3	1122	1	FKMUA	phytochrome A - Arabi	2.93e-159
18	864	59.3	1124	2	S06856	phytochrome - garden	4.89e-159
19	865	59.3	1129	2	S52631	phytochrome A - parsl	2.93e-159
20	847	58.1	1129	2	A29631	phytochrome - oat	2.94e-155
21	845	58.0	495	2	S00098	phytochrome 5 - oat (	8.17e-155
22	845	58.0	1129	2	S00097	phytochrome 4 - oat	8.17e-155
23	837	57.4	1129	2	S00096	phytochrome 3 - oat	4.89e-153
24	836	57.3	1128	2	S03728	phytochrome (clone ph	8.15e-153
25	831	57.0	1131	2	JQ0382	phytochrome A - maize	1.05e-151
26	773	53.0	190	2	S46926	phytochrome - Marsile	7.40e-139
27	718	49.2	189	2	S46927	phytochrome - Nymphae	1.00e-126
28	594	40.7	197	2	S46928	phytochrome - Chara f	1.34e-99
29	552	37.9	748	1	S74389	phytochrome phy - Syn	1.68e-90
30	487	33.4	103	2	S62718	phytochrome E - tomat	1.55e-76
31	404	27.7	87	2	S62719	phytochrome F - tomat	5.76e-59
32	395	27.1	103	2	S62715	phytochrome A - tomat	4.40e-57
33	275	18.9	794	2	S37158	phytochrome - whisk f	1.41e-32
34	266	18.2	1276	2	S75801	hypothetical protein	8.45e-31
35	188	12.9	114	2	PQ0745	phytochrome - Mesotae	5.93e-16
36	129	8.8	76	2	A60685	phytochrome II - gard	8.13e-06
37	116	8.0	481	2	S76820	hypothetical protein	8.39e-04
38	108	7.4	844	2	S77547	ethylene response sen	1.28e-02
39	105	7.2	422	2	F70018	multiple sugar-bindin	3.45e-02
40	105	7.2	715	2	B70741	probable moeY protein	3.45e-02
41	104	7.1	407	2	A40150	inhibin beta-B chain	4.78e-02
42	102	7.0	255	2	I48235	inhibin beta-B chain	9.14e-02
43	102	7.0	411	2	B41398	inhibin beta-B chain	9.14e-02
44	101	6.9	577	2	S62713	phytochrome 1a - Meso	1.26e-01
45	101	6.9	874	2	H64228	DNA polymerase III al	1.26e-01

ALIGNMENTS

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RESULT    1
ENTRY           S46313     #type complete
TITLE           phytochrome E - Arabidopsis thaliana
ORGANISM        #formal_name Arabidopsis thaliana #common_name mouse-ear
                  cress
DATE            27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change
                  01-May-1998
ACCESSIONS      S46313; S41912
REFERENCE       S46312
   #authors     Clack, T.; Mathews, S.; Sharrock, R.A.
   #journal     Plant Mol. Biol. (1994) 25:413-427
   #title       The phytochrome apoprotein family in Arabidopsis is encoded
                  by five genes: the sequences and expression of PHYD and
                  PHYE.
   #cross-references MUID:94325466
   #accession   S46313
      ##molecule_type DNA
      ##residues      1-1112 ##label CLA
      ##cross-references EMBL:X76610; NID:g452815; PID:g452817
GENETICS
   #gene        PHYE
CLASSIFICATION  #superfamily phytochrome; phytochrome homology
KEYWORDS        phytochromobilin
FEATURE
   63-569            #domain phytochrome homology #label PHYT\
   322               #binding_site phytochromobilin (Cys) (covalent) #status
                       predicted
SUMMARY         #length 1112  #molecular-weight 122587  #checksum 9259

  Query Match          100.0%;  Score 1458;  DB 2;  Length 1112;
  Best Local Similarity 100.0%;  Pred. No. 9.32e-293;
  Matches   196;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db    201 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL 260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL 60

Db    261 EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     61 EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120

Db    321 GCHTQYMANMGSVASLALAIVVKGKDSSKLWGLVVGHHCSPRYVPFPLRYACEFLMQAFG 380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    121 GCHTQYMANMGSVASLALAIVVKGKDSSKLWGLVVGHHCSPRYVPFPLRYACEFLMQAFG 180

Db    381 LQLQMELQLASQLAEK 396
          ||||||||||||||||
```

```
Qy    181 LQLQMELQLASQLAEK 196


RESULT    2
ENTRY             T03668     #type complete
TITLE             phytochrome B - common tobacco
ORGANISM          #formal_name Nicotiana tabacum #common_name common tobacco
DATE              24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change
                    24-Mar-1999
ACCESSIONS        T03668
REFERENCE         Z14996
   #authors       Kern, R.; Gasch, A.; Deak, M.; Kay, S.A.; Chua, N.H.
   #journal       Plant Physiol. (1993) 102:1363-1364
   #title         PhyB of tobacco, a new member of the photoreceptor family.
   #accession     T03668
      ##status         preliminary; translated from GB/EMBL/DDBJ
      ##molecule_type DNA
      ##residues       1-1132 ##label KER
      ##cross-references EMBL:L10114; NID:g295345; PID:g295346
      ##experimental_source strain SR1; tissue-type etiolated seedling
GENETICS
   #gene          phyB
CLASSIFICATION    #superfamily phytochrome; phytochrome homology
KEYWORDS          photoreceptor; phytochromobilin
SUMMARY           #length 1132  #molecular-weight 125808  #checksum 502

  Query Match            78.4%;  Score 1143;  DB 2;  Length 1132;
  Best Local Similarity  77.0%;  Pred. No. 1.65e-221;
  Matches   157;  Conservative   25;  Mismatches  14;  Indels   8;  Gaps   2;

Db    215 KLAVRAISHLQSLPGGDVKLLCDTVVESVRELTGYDRVMVYKFHEDEHGEVVAESKIPDL 274
          ||||||||:||||||||:  ||||||| |: |||||||||| ||||:|||||:| : :||
Qy      1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL 60

Db    275 EPYIGLHYPATDIPQASRFLFKQNRVRMIVDCHATPVRVVQDESLMQPLCLVGSTLRAPH 334
          |#|:|||||||||||||:|||||||||||| ||:||||:||| | |::||||| |||||||
Qy     61 EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120

Db    335 GCHAQYMANMGSIASLTLAVIINGNDEEAVGGRSSMRLWGLVVGHHTSARCIPFPLRYAC 394
          |||:||||||||:|||:||:::::|:|       || :|||||||| |:| :||||||||
Qy    121 GCHTQYMANMGSVASLALAIVVKGKD-------SS-KLWGLVVGHHCSPRYVPFPLRYAC 172

Db    395 EFLMQAFGLQLNMELQLASQLSEK 418
          |||||||||| |||||||||:||
Qy    173 EFLMQAFGLQLQMELQLASQLAEK 196


RESULT    3
ENTRY             FKMUB      #type complete
TITLE             phytochrome B - Arabidopsis thaliana
ORGANISM          #formal_name Arabidopsis thaliana #common_name mouse-ear
                    cress
DATE              30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change
                    20-Feb-1998
ACCESSIONS        B33473; JQ2141; S07718
REFERENCE         A33473
   #authors       Sharrock, R.A.; Quail, P.H.
   #journal       Genes Dev. (1989) 3:1745-1757
   #title         Novel phytochrome sequences in Arabidopsis thaliana:
                    structure, evolution, and differential expression of a
                    plant regulatory photoreceptor family.
   #cross-references MUID:90108670
   #accession     B33473
      ##molecule_type mRNA
      ##residues       1-1172 ##label SHA
      ##cross-references EMBL:X17342; NID:g16422; PID:g16423
REFERENCE         JQ2141
   #authors       Reed, J.W.; Nagpal, P.; Poole, D.S.; Furuya, M.; Chory, J.
   #journal       Plant Cell (1993) 5:147-157
   #title         Mutations in the gene for the red/far-red light receptor
                    phytochrome B alter cell elongation and physiological
                    responses throughout Arabidopsis development.
   #accession     JQ2141
      ##molecule_type DNA
      ##residues       1-1172 ##label REE
      ##cross-references GB:L09262
      ##experimental_source ecotype Landsberg, mutant hy3
GENETICS
   #gene          phyB
   #introns       722/1; 991/2; 1088/2
CLASSIFICATION    #superfamily phytochrome; phytochrome homology
KEYWORDS          dimer; photoreceptor; phytochromobilin; transcription
                    regulation
FEATURE
   101-614             #domain phytochrome homology #label PHYT\
   901-1172            #domain signal transduction #label STD\
   357                 #binding_site phytochromobilin (Cys) (covalent) #status
                         predicted
SUMMARY           #length 1172  #molecular-weight 129330  #checksum 6013

  Query Match            73.4%;  Score 1070;  DB 1;  Length 1172;
  Best Local Similarity  73.9%;  Pred. No. 4.30e-205;
  Matches   153;  Conservative   25;  Mismatches  18;  Indels  11;  Gaps   3;

Db    236 KLAVRAISQLQALPGGDIKLLCDTVVESVRDLTGYDRVMVYKFHEDEHGEVVAESKRDDL 295
          ||||||||:||:||||||  ||||||| |: |||||||||| ||||:|||||:| :| ||
Qy      1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL 60

Db    296 EPYIGLHYPATDIPQASRFLFKQNRVRMIVDCNATPVLVVQDDRLTQSMCLVGSTLRAPH 355
          |||:||||||||||||:|||||||||||| ||||||| ||| : | :::||| |||||||
Qy     61 EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120

Db    356 GCHSQYMANMGSIASLAMAVIINGNEDDGSNVASGRSSMRLWGLVVCHHTSSRCIPFPLR 415
          |||:||||||||:||||:|::::|:  |        || :|||||| || |:| :|||||
Qy    121 GCHTQYMANMGSVASLALAIVVKGK--D--------SS-KLWGLVVGHHCSPRYVPFPLR 169

Db    416 YACEFLMQAFGLQLNMELQLALQMSEK 442
          |||||||||||||| |||||| |::||
Qy    170 YACEFLMQAFGLQLQMELQLASQLAEK 196


RESULT    4
ENTRY             S14065     #type complete
TITLE             phytochrome B - rice
ORGANISM          #formal_name Oryza sativa #common_name rice
DATE              19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change
                    26-Feb-1999
ACCESSIONS        S14065
REFERENCE         S14065
   #authors       Dehesh, K.; Tepperman, J.; Christensen, A.H.; Quail, P.H.
   #journal       Mol. Gen. Genet. (1991) 225:305-313
   #title         phyB is evolutionarily conserved and constitutively expressed
                    in rice seedling shoots.
   #cross-references MUID:91172131
   #accession     S14065
      ##status         preliminary
      ##molecule_type DNA
      ##residues       1-1171 ##label DEH
GENETICS
   #gene          phyB
CLASSIFICATION    #superfamily phytochrome; phytochrome homology
KEYWORDS          photoreceptor; phytochromobilin; transcription regulation
FEATURE
   103-623             #domain phytochrome homology #label PHYT\
   364                 #binding_site phytochromobilin (Cys) (covalent) #status
                         predicted
SUMMARY           #length 1171  #molecular-weight 128384  #checksum 8692

  Query Match            73.1%;  Score 1066;  DB 2;  Length 1171;
  Best Local Similarity  72.7%;  Pred. No. 3.40e-204;
  Matches   152;  Conservative   23;  Mismatches  21;  Indels  13;  Gaps   4;

Db    243 KLVVRAISRLQALPGGDVKLLCDTVVEHVRELTGYDRVMVYRFHEDEHGEVVAESRRSNL 302
          || |||||||:|||||:  ||||||| |: |||||||||:||||:|||||:| |||:|
Qy      1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL 60
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```
Db    303 EPYIGLHYPATDIPQASRFLFRQNRVRMIADCHAAPVRVIQDPALTQPLCLVGSTLRSPH 362
          |||:|||||||||||||:||||:||||||| ||:|:||:|:|   | :||||| ||||:||
Qy     61 EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120

Db    363 GCHGQYMANMGSIASLVMAVIISSGGDDDHNIARGSIPSAMKLWGLVVCHHTSPRCIPFP 422
          ||| |||||||||||| :|::::   | |       |  |  ||||||| || ||| :|||
Qy    121 GCHTQYMANMGSVASLALAIVVK--GKD-------S--S--KLWGLVVGHHCSPRYVPFP 167

Db    423 LRYACEFLMQAFGLQLNMELQLAHQLSEK 451
          |||||||||||||||| |||||| ||:||
Qy    168 LRYACEFLMQAFGLQLQMELQLASQLAEK 196


RESULT    5
ENTRY             B71429     #type complete
TITLE             phytochrome D - Arabidopsis thaliana
ORGANISM          #formal_name Arabidopsis thaliana #common_name mouse-ear
                    cress
   #variety       columbia
DATE              03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change
                    26-Feb-1999
ACCESSIONS        B71429; S46312; S41910
REFERENCE         A71400
   #authors       Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.;
                    Dean, C.; Bergkamp, R.; Dirkse, W.; Van Staveren, M.;
                    Stiekema, W.; Drost, L.; Ridley, P.; Hudson, S.A.; Patel,
                    K.; Murphy, G.; Piffanelli, P.; Wedler, H.; Wedler, E.;
                    Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.;
                    Gielen, J.; Villarroel, R.; De Clerck, R.; Van Montagu, M.;
                    Lecharny, A.; Auborg, S.; Gy, I.; Kreis, M.; Lao, N.;
                    Kavanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger,
                    M.; Schaeffer, M.; Funk, B.; Mueller-Auer, S.; Silvey, M.;
                    James, R.; Montfort, A.; Pons, A.; Puigdomenech, P.; Douka,
                    A.; Voukelatou, E.; Milioni, D.; Hatzopoulos, P.;
                    Piravandi, E.; Obermaier, B.; Hilbert, H.; Duesterhoft, A.;
                    Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.;
                    Rechman, S.; Ansorge, W.; Cooke, R.; Berger, C.; Delseny,
                    M.; Voet, M.; Volckaert, G.; Mewes, H.W.; Klosterman, S.;
                    Schueller, C.; Chalwatzis, N.
   #journal       Nature (1998) 391:485-488
   #title         Analysis of 1.9 Mb of contiguous sequence from chromosome 4
                    of Arabidopsis thaliana.
   #cross-references MUID:98121113
   #accession     B71429
      ##status        preliminary; nucleic acid sequence not shown;
                        translation not shown
      ##molecule_type DNA
      ##residues      1-1164 ##label BEV
      ##cross-references GB:Z97340; NID:g2244950; PID:e326982; PID:g2244983
REFERENCE         S46312
   #authors       Clack, T.; Mathews, S.; Sharrock, R.A.
   #journal       Plant Mol. Biol. (1994) 25:413-427
   #title         The phytochrome apoprotein family in Arabidopsis is encoded
                    by five genes: the sequences and expression of PHYD and
                    PHYE.
   #cross-references MUID:94325466
   #accession     S46312
      ##molecule_type DNA
      ##residues      1-424,'F',426-1164 ##label CLA
      ##cross-references EMBL:X76609; NID:g452812; PID:g452814
GENETICS
   #gene          PHYD
   #map_position 4COP9-4G3845
CLASSIFICATION    #superfamily phytochrome; phytochrome homology
KEYWORDS          photoreceptor; phytochromobilin; transcription regulation
FEATURE
   103-618             #domain phytochrome homology #label PHYT\
   360                 #binding_site phytochromobilin (Cys) (covalent) #status
                         predicted
SUMMARY           #length 1164  #molecular-weight 129267  #checksum 4171

  Query Match           71.3%;  Score 1039;  DB 2;  Length 1164;
  Best Local Similarity 71.6%;  Pred. No. 3.90e-198;
  Matches  149;  Conservative   29;  Mismatches  18;  Indels  12;  Gaps   4;

Db    239 KLAVRAISHLQSLPSGDIKLLCDTVVESVRDLTGYDRVMVYKFHEDEHGEVVAESKRNDL 298
          ||||||||:|||||:|||  |||||||  |: |||||||||| ||||:|||||:| :|:||
Qy      1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL 60

Db    299 EPYIGLHYPATDIPQASRFLFKQNRVRMIVDCYASPVRVVQDDRLTQFICLVGSTLRAPH 358
          |||:|||||||||||||:|||||||||||| || |:||:||| : | : :||| |||||||
Qy     61 EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120

Db    359 GCHAQYMTNMGSIASLAMAVIINGNEEDGNGVNTGGRNSMRLWGLVVCHHTSARCIPFPL 418
          |||:|||:||||:||||:|::::|:  |     :    | :|||||| || |:| :||||
Qy    121 GCHTQYMANMGSVASLALAIVVKGK--D-----S----S-KLWGLVVGHHCSPRYVPFPL 168

Db    419 RYACEFLMQAFGLQLNMELQLALQVSEK 446
          |||||||||||||| |||||| |::||
Qy    169 RYACEFLMQAFGLQLQMELQLASQLAEK 196


RESULT    6
ENTRY             S58130     #type fragment
TITLE             phytochrome - moss (Ceratodon purpureus) (fragment)
ORGANISM          #formal_name Ceratodon purpureus
DATE              13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change
                    01-May-1998
ACCESSIONS        S58130
REFERENCE         S58129
   #authors       Hughes, J.; Mittmann, F.
   #submission    submitted to the EMBL Data Library, July 1995
   #description   The moss Ceratodon purpureus contains and expresses a second,
                    conventional like phytochrome gene.
   #accession     S58130
      ##status        preliminary
      ##molecule_type DNA
      ##residues      1-577 ##label HUG
      ##cross-references EMBL:X89725
CLASSIFICATION    #superfamily phytochrome; phytochrome homology
KEYWORDS          phytochromobilin
FEATURE
   63-574              #domain phytochrome homology #label PHYT\
   319                 #binding_site phytochromobilin (Cys) (covalent) #status
                         predicted
SUMMARY           #length 577  #checksum 2846

  Query Match           70.6%;  Score 1030;  DB 2;  Length 577;
  Best Local Similarity 69.3%;  Pred. No. 4.07e-196;
  Matches  142;  Conservative   31;  Mismatches  23;  Indels   9;  Gaps   3;

Db    198 KLAAKAITRLQALPGGDIGLLCDTVVEEVRELTGYDRVMAYKFHEDEHGEVVAEIRRMDL 257
          ||| :||:|||:||||||| ||||||||:|: |||||||| | ||||:|||||:|||| ||
Qy      1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL 60

Db    258 EPYLGLHYPATDIPQASRFLFMKNRVRVIADCCASPVKLIQDPDIKQPVSLAGSTLRAPH 317
          |||||||||||||||||:||||: ||||:| || |:|||::|  ::|:|: |  |||||||
Qy     61 EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120

Db    318 GCHAQYMGNMGSIASLVMAVIINDNEEDSRGAIQRGRKLWGLVVCHHTSPRTVPFPLRSA 377
          |||:|||:||||:||| :|:::: :  ||  :     ||||||| || ||| |||||| |
Qy    121 GCHTQYMANMGSVASLALAIVVKGK--DS--S-----KLWGLVVGHHCSPRYVPFPLRYA 171

Db    378 CEFLMQVFGMQLNMEVELAAQLREK 402
          |||||| ||:|| ||::||:|| ||
Qy    172 CEFLMQAFGLQLQMELQLASQLAEK 196


RESULT    7
ENTRY             S28431     #type complete
TITLE             phytochrome B - potato
ORGANISM          #formal_name Solanum tuberosum #common_name potato
DATE              07-May-1993 #sequence_revision 07-May-1993 #text_change
                    01-May-1998
ACCESSIONS        S28431
REFERENCE         S28431
```

```
  #authors      Heyer, A.; Gatz, C.
  #journal      Plant Mol. Biol. (1992) 20:589-600
  #title        Isolation and characterization of a cDNA-clone coding for
                potato type B phytochrome.
  #cross-references MUID:93081720
  #accession    S28431
    ##status        not compared with conceptual translation
    ##molecule_type mRNA
    ##residues      1-1129 ##label HEY
GENETICS
  #gene         phyB
CLASSIFICATION  #superfamily phytochrome; phytochrome homology
KEYWORDS        photoreceptor; phytochromobilin; transcription regulation
FEATURE
  76-588             #domain phytochrome homology #label PHYT\
  333                #binding_site phytochromobilin (Cys) (covalent) #status
                      predicted
SUMMARY         #length 1129  #molecular-weight 125621  #checksum 8608

  Query Match           70.4%;  Score 1027;  DB 2;  Length 1129;
  Best Local Similarity  74.7%;  Pred. No. 1.92e-195;
  Matches   142;  Conservative   23;  Mismatches  16;  Indels   9;  Gaps   3;

Db    227 GTLKLLCDTVVESVRELTGYDRVMVYKFHEDEHGEVVAESKRSDLEPYIGLHYPATDIPQ 286
          | :  ||||||| |: |||||||||| ||||:|||||:| :|||||||:||||||||||
Qy     16 GDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDLEPYLGLHYPATDIPQ 75

Db    287 ASRFLFKQNRVRMIVDCHATPVRVTQDESLMQPLCLVGSTLRAPHGCHAQYMANMGSIAS 346
          |:|||||||||| ||:||||:| | | |::||||| ||||||||||:||||||||:||
Qy     76 AARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPHGCHTQYMANMGSVAS 135

Db    347 LTLAVIINGNDEEAVGGGRNSMRLWGLVVGHHTSVRSIPFPLRYACEFLMQAFGLQLNME 406
          |:||::::|:|  :      | :|||||||| | | :|||||||||||||||||| ||
Qy    136 LALAIVVKGKD--S------S-KLWGLVVGHHCSPRYVPFPLRYACEFLMQAFGLQLQME 186

Db    407 LQLASQLSEK 416
          |||||||:||
Qy    187 LQLASQLAEK 196


RESULT    8
ENTRY           S62714     #type complete
TITLE           phytochrome 1b - Mesotaenium caldariorum
ORGANISM        #formal_name Mesotaenium caldariorum
DATE            19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change
                  15-Jan-1999
ACCESSIONS      S62714
REFERENCE       S62713
  #authors      Lagarias, D.M.; Wu, S.H.; Lagarias, J.C.
  #journal      Plant Mol. Biol. (1995) 29:1127-1142
  #title        Atypical phytochrome gene structure in the green alga
                  Mesotaenium caldariorum.
  #cross-references MUID:96191280
  #accession    S62714
    ##molecule_type DNA
    ##residues      1-1142 ##label LAG
    ##cross-references EMBL:U31284; NID:g1125698; PID:g1125699
GENETICS
  #introns      125/1; 298/3; 393/3; 468/3; 543/2; 621/3; 699/1; 785/1;
                  856/3; 970/2; 1067/2
CLASSIFICATION  #superfamily phytochrome; phytochrome homology
KEYWORDS        photoreceptor; phytochromobilin; transcription regulation
FEATURE
  68-589             #domain phytochrome homology #label PHYT\
  880-1139           #domain signal transduction #status predicted #label
                      STD\
  324                #binding_site phytochromobilin (Cys) (covalent) #status
                      predicted
SUMMARY         #length 1142  #molecular-weight 125028  #checksum 6173

  Query Match           69.9%;  Score 1019;  DB 2;  Length 1142;
  Best Local Similarity  69.5%;  Pred. No. 1.19e-193;
  Matches   146;  Conservative   28;  Mismatches  22;  Indels  14;  Gaps   3;

Db    203 KLAAKAISRLQSLPGGDIGLLCDAVVEEVRELTGYDRVMAYKFHEDEHGEVIAEIRRSDL 262
          ||| :|||||||||||||| |||:|||:|: |||||||| | ||||:||||::|||||||
Qy      1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL 60

Db    263 EPYLGLHYPATDIPQAARFLFMKNRVRIICDCSAPPVKVIQDPTMKHPISLAGSTLRGVH 322
          |||||||||||||||||||: ||||:||||:| ||||:|   :|:|: |  ||||: |
Qy     61 EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120

Db    323 GCHAQYMANMGSVASLVMAVIINDNSSEEGATAAGGILHKGRKLWGLVVCHHSSPRYVPF 382
          |||:|||||||||| :|:::: :   :   ::        ||||||| || |||||||
Qy    121 GCHTQYMANMGSVASLALAIVVKGK---D---SS--------KLWGLVVGHHCSPRYVPF 166

Db    383 PLRSACEFLMQVFGLQLNMEVELSSQLREK 412
          ||| ||||||| ||||| ||::|:||| ||
Qy    167 PLRYACEFLMQAFGLQLQMELQLASQLAEK 196


RESULT    9
ENTRY           S37206     #type complete
TITLE           phytochrome - moss (Physcomitrella patens)
ORGANISM        #formal_name Physcomitrella patens
DATE            13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
                  17-Mar-1999
ACCESSIONS      S37206; S39070
REFERENCE       S37206
  #authors      Kolukisaoglu, H.U.; Braun, B.; Schneider-Poetsch, H.J.A.W.
  #submission   submitted to the EMBL Data Library, September 1993
  #description  Evidence that mosses do express conventional B-type related
                  phytochromes Phytochrome of Physcomitrella patens (Hedw.).
  #accession    S37206
    ##molecule_type mRNA
    ##residues      1-1132 ##label KOL
    ##cross-references EMBL:X75025; NID:g402605; PID:g402606
REFERENCE       S39070
  #authors      Kolukisaoglu, H.U.; Braun, B.; Martin, W.F.;
                  Schneider-Poetsch, H.A.W.
  #journal      FEBS Lett. (1993) 334:95-100
  #title        Mosses do express conventional, distantly B-type-related
                  phytochromes. Phytochrome of Physcomitrella patens (Hedw.).
  #cross-references MUID:94039823
  #accession    S39070
    ##status        preliminary
    ##molecule_type mRNA
    ##residues      1-118,'M',120-1132 ##label KO2
    ##cross-references EMBL:X75025
CLASSIFICATION  #superfamily phytochrome; phytochrome homology
KEYWORDS        photoreceptor; phytochromobilin; transcription regulation
FEATURE
  65-576             #domain phytochrome homology #label PHYT\
  321                #binding_site phytochromobilin (Cys) (covalent) #status
                      predicted
SUMMARY         #length 1132  #molecular-weight 125230  #checksum 7632

  Query Match           69.7%;  Score 1016;  DB 2;  Length 1132;
  Best Local Similarity  67.8%;  Pred. No. 5.60e-193;
  Matches   139;  Conservative   33;  Mismatches  24;  Indels   9;  Gaps   3;

Db    200 KLAAKAITRLQALPGGNIGLLCDTVVEEVRELTGYDRVMAYRFHEDEHGEVVAEIRRADL 259
          ||| :||:|||:||||:|| |||||||:|: |||||||| |:||||:|||||:||||:||
Qy      1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL 60

Db    260 EPYLGLHYPGTDIPQASRFLFMKNKVRIIADCSAPPVKVIQDPTLRQPVSLAGSTLRSPH 319
          |||||||||:||||||:|||||: |:||:| ||:| ||||:|   |::|: |  ||||:||
Qy     61 EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120

Db    320 GCHAQYMGNMGSIASLVMAVIINDNEEDSHGSVQRGRKLWGLVVCHHTSPRTVPFPLRSA 379
          |||:|||:||||:||| :|:::: :  ||  |     ||||||| || ||| |||||| |
Qy    121 GCHTQYMANMGSVASLALAIVVKGK--DS--S-----KLWGLVVGHHCSPRYVPFPLRYA 171

Db    380 CGFLMQVFGLQLNMEVESAAQLREK 404
          | |||| ||||| ||:: |:||| ||
Qy    172 CEFLMQAFGLQLQMELQLASQLAEK 196
```

```
RESULT   10
ENTRY            S27396     #type complete
TITLE            phytochrome / protein kinase (EC 2.7.1.-) - moss (Ceratodon
                   purpureus)
ORGANISM         #formal_name Ceratodon purpureus
DATE             28-May-1993 #sequence_revision 28-May-1993 #text_change
                   19-Dec-1998
ACCESSIONS       S27396; S20160; S12966
REFERENCE        S27396
   #authors      Thuemmler, F.; Dufner, M.; Kreisl, P.; Dittrich, P.
   #journal      Plant Mol. Biol. (1992) 20:1003-1017
   #title        Molecular cloning of a novel phytochrome gene of the moss
                   Ceratodon purpureus which encodes a putative
                   light-regulated protein kinase.
   #accession    S27396
      ##molecule_type DNA
      ##residues      1-1303 ##label THU
      ##cross-references GB:S51224
REFERENCE        S20160
   #authors      Thuemmler, F.; Dufner, M.; Kreisl, P.; Dittrich, P.
   #submission   submitted to the Protein Sequence Database, April 1992
   #description  Molecular cloning of a novel phytochrome gene of the moss
                   Ceratodon purpureus which encodes a putative light
                   regulated protein kinase.
   #accession    S20160
      ##molecule_type DNA
      ##residues      1-1303 ##label TH2
REFERENCE        S12966
   #authors      Thuemmler, F.; Beetz, A.; Ruediger, W.
   #journal      FEBS Lett. (1990) 275:125-129
   #title        Phytochrome in lower plants. Detection and partial sequence
                   of a phytochrome gene in the moss Ceratodon purpureus using
                   the polymerase chain reaction.
   #cross-references MUID:91085543
   #accession    S12966
      ##molecule_type DNA
      ##residues      49-539 ##label FEB
GENETICS
   #gene         phy
   #introns      679/1; 779/1
CLASSIFICATION   #superfamily phytochrome / protein kinase; phytochrome
                   homology; protein kinase homology
KEYWORDS         ATP; phosphotransferase; photoreceptor; phytochromobilin;
                   serine/threonine-specific protein kinase; transcription
                   regulation

FEATURE
   63-575             #domain phytochrome homology #label PHYT\
   1002-1289          #domain protein kinase homology #label KIN\
   320                #binding_site phytochromobilin (Cys) (covalent) #status
                        predicted
SUMMARY          #length 1303  #molecular-weight 145369  #checksum 4924

  Query Match           67.6%;  Score 986;  DB 2;  Length 1303;
  Best Local Similarity  64.4%;  Pred. No. 2.93e-186;
  Matches   132;  Conservative   38;  Mismatches  26;  Indels   9;  Gaps   3;

Db    199 KLAARAITRLQALPGGDIELLCDTIVEEVRELTGYDRVMAFKFHEDEHGEVVAEIRRMDL 258
          ||| |||:|||:|||||| ||||:||:|: |||||||| : ||||:|||||:|||| ||
Qy      1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL 60

Db    259 EPYMGLHYPATDIPQASRFLLMKNRVRLIADCYASPVKLIQDPDIRQPVSLAGSTLRAPH 318
          |||:||||||||||||:|||:: ||||:| || |:|||::|  ::::|: |  ||||||||
Qy     61 EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120

Db    319 GCHAQYMGNMGSIASLVMAVIINDNEEYSRGAIQRGRKLWGLVVCQHTSPRTVPFPLRSV 378
          |||:|||:||||:||| :|:::: ::  |  :     ||||||| :| ||| ||||||
Qy    121 GCHTQYMANMGSVASLALAIVVKGKD--S--S-----KLWGLVVGHHCSPRYVPFPLRYA 171

Db    379 CEFLMQVFGMQLNLHVELAAQLREK 403
          |||||| ||:|| : ::||:|| ||
Qy    172 CEFLMQAFGLQLQMELQLASQLAEK 196
```

```
RESULT   11
ENTRY            S31280     #type complete
TITLE            phytochrome - Martens's spike moss
ORGANISM         #formal_name Selaginella martensii #common_name Martens's
                   spike moss
DATE             30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
                   17-Mar-1999
ACCESSIONS       S31280; S25401
REFERENCE        S31280
   #authors      Hanelt, S.; Braun, B.; Marx, S.; Schneider-Poetsch, H.A.W.
   #journal      Photochem. Photobiol. (1992) 56:751-758
   #title        Phytochrome evolution: a phylogenetic tree with the first
                   complete sequence of phytochrome from a cryptogamic plant
                   (Selaginella martensii Spring).
   #cross-references MUID:93117303
   #accession    S31280
      ##molecule_type DNA
      ##residues      1-1134 ##label HAN
      ##cross-references EMBL:X61458; NID:g22602; PID:g22603
      ##note          the authors translated the codon CTG for residue 239 as
                       Arg, CAC for residue 524 as Ala, and GAC for residue
                       742 as Glu
REFERENCE        S25401
   #authors      Schneider-Poetsch, H.A.W.; Braun, B.
   #journal      Plant Physiol. (1991) 137:576-580
   #title        Proposal on the nature of phytochrome action based on the
                   C-terminal sequences of phytochrome.
   #accession    S25401
      ##molecule_type mRNA
      ##residues      'L',730-899,'GLHPP',905-936,'T',938-1134 ##label SCH
GENETICS
   #introns      686/1; 958/2; 1056/2
CLASSIFICATION   #superfamily phytochrome; phytochrome homology
KEYWORDS         photoreceptor; phytochromobilin; transcription regulation
FEATURE
   66-582             #domain phytochrome homology #label PHYT\
   324                #binding_site phytochromobilin (Cys) (covalent) #status
                        predicted
SUMMARY          #length 1134  #molecular-weight 124706  #checksum 3030

  Query Match           66.5%;  Score 969;  DB 2;  Length 1134;
  Best Local Similarity  68.9%;  Pred. No. 1.86e-182;
  Matches   144;  Conservative   26;  Mismatches  25;  Indels  14;  Gaps   4;

Db    203 KLAAKAISRLQSLPGGDIGLLCDTVVEEVRDVTGYDLVMAYKFHEDEHGEVVAEIRRSDL 262
          ||| :|||||||||||||| |||||||:|: :|||| || | ||||:|||||:|||||||
Qy      1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL 60

Db    263 EPYLGLHYPATDIPQASRFLFMKNRVRMICDCSAPPVKITQDKELRQPISLAGSTLRAPH 322
          |||||||||||||||:||||: |||||||||:| |||: |  ||::|: |  |||||||
Qy     61 EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120

Db    323 GCHAQYMGNMGSVASLVMAMIINDNDEPSGGGGGGGQHKGRRLWGLVVCHHTSPRSVPF- 381
          |||:|||:|||||||| :|:::: :|  |:        |   |||||| || ||| |||
Qy    121 GCHTQYMANMGSVASLALAIVVKGKD--SS--------K---LWGLVVGHHCSPRYVPFP 167

Db    382 LRSACEFLMQVFGLQLNMEAAVAAHVREK 410
          || ||||||| ||||| ||  :|::: ||
Qy    168 LRYACEFLMQAFGLQLQMELQLASQLAEK 196


RESULT   12
ENTRY            S62721     #type fragment
TITLE            phytochrome B2 - tomato (fragment)
ORGANISM         #formal_name Lycopersicon esculentum #common_name tomato
DATE             19-Mar-1997 #sequence_revision 23-Aug-1997 #text_change
                   01-May-1998
ACCESSIONS       S62721; S62717
REFERENCE        S62720
   #authors      Hauser, B.A.; Cordonnier-Pratt, M.M.; Daniel-Vedele, F.;
                   Pratt, L.H.
```

```
   #submission   submitted to the EMBL Data Library, July 1995
   #description  The phytochrome gene family in tomato includes a novel
                   subfamily.
   #accession    S62721
      ##molecule_type DNA
      ##residues      1-210 ##label HAU
      ##cross-references EMBL:U32442
REFERENCE        S62715
   #authors      Hauser, B.A.; Cordonnier-Pratt, M.M.; Daniel-Vedele, F.;
                   Pratt, L.H.
   #journal      Plant Mol. Biol. (1995) 29:1143-1155
   #title        The phytochrome gene family in tomato includes a novel
                   subfamily.
   #cross-references MUID:96191281
   #accession    S62717
      ##status       nucleic acid sequence not shown
      ##molecule_type DNA
      ##residues      1-108 ##label HAW
      ##cross-references EMBL:U32442
CLASSIFICATION   #superfamily phytochrome; phytochrome homology
KEYWORDS         photoreceptor; phytochromobilin
FEATURE
   154               #binding_site phytochromobilin (Cys) (covalent) #status
                       predicted
SUMMARY          #length 210  #checksum 7739

  Query Match            66.0%;  Score 963;  DB 2;  Length 210;
  Best Local Similarity  73.6%;  Pred. No. 4.09e-181;
  Matches   131;  Conservative   22;  Mismatches  17;  Indels   8;  Gaps   2;

Db      33 KLAVRAISLLQSLPGGDIDLLCDTVVKSVRELTGYDRVMVYKFHDDEHGEVVAESRRSDL 92
           |||||||| |||||||||  ||||||  |: |||||||||| ||:|:|||||:| |||||
Qy       1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL 60

Db      93 EPYIGLHYPATDIPQASRFLFKQNRVRMIVDCTAIPVRVIQDESLMQPLCLVGSTLRAPH 152
           |||:||||||||||||:|||||||||||| || | ||:|:| | |::||||| |||||||
Qy      61 EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120

Db     153 GCHPQYMVNMGNVASLTLAVVINGNDDEVVGGRNAMRLWGLVVGHHSSARFIPFPLRY 210
           ||| ||| |||:||||:||:|::|:|       :: :||||||||| |:|::||||||
Qy     121 GCHTQYMANMGSVASLALAIVVKGKD-------SS-KLWGLVVGHHCSPRYVPFPLRY 170


RESULT   13
ENTRY            S62720     #type fragment
TITLE            phytochrome B1 - tomato (fragment)
ORGANISM         #formal_name Lycopersicon esculentum #common_name tomato
DATE             27-Apr-1996 #sequence_revision 07-Feb-1997 #text_change
                   12-Feb-1999
ACCESSIONS       S62720; S62716
REFERENCE        S62720
   #authors      Hauser, B.A.; Cordonnier-Pratt, M.M.; Daniel-Vedele, F.;
                   Pratt, L.H.
   #submission   submitted to the EMBL Data Library, July 1995
   #description  The phytochrome gene family in tomato includes a novel
                   subfamily.
   #accession    S62720
      ##molecule_type DNA
      ##residues      1-211 ##label HAU
      ##cross-references EMBL:U32441
REFERENCE        S62715
   #authors      Hauser, B.A.; Cordonnier-Pratt, M.M.; Daniel-Vedele, F.;
                   Pratt, L.H.
   #journal      Plant Mol. Biol. (1995) 29:1143-1155
   #title        The phytochrome gene family in tomato includes a novel
                   subfamily.
   #cross-references MUID:96191281
   #accession    S62716
      ##status       nucleic acid sequence not shown
      ##molecule_type DNA
      ##residues      1-108 ##label HAW
      ##cross-references EMBL:U32441
CLASSIFICATION   #superfamily phytochrome; phytochrome homology
KEYWORDS         photoreceptor; phytochromobilin
FEATURE
   154               #binding_site phytochromobilin (Cys) (covalent) #status
                       predicted
SUMMARY          #length 211  #checksum 274

  Query Match            65.0%;  Score 948;  DB 2;  Length 211;
  Best Local Similarity  74.3%;  Pred. No. 9.21e-178;
  Matches   133;  Conservative   23;  Mismatches  14;  Indels   9;  Gaps   3;

Db      33 KLAVRAISHLQSLPGGDIKLLCDTVVESVRELTGYDRVMVYKFHEDEHGEVVAESKRSDL 92
           ||||||||:|||||||||  |||||||  |: |||||||||| ||||:|||||:| :||||
Qy       1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL 60

Db      93 EPYIGLHYPATDIPQASRFLFKQNRVRMVVDCHATPVRVTQDESLMQPLCLVGSTLRAPH 152
           |||:|||||||||||:|||||||||||: ||:||||:| | | |::||||| |||||||
Qy      61 EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120

Db     153 GCHAQYMANMGSIASLTLAVIINGNDEEAVGGGRNSMRLWGLVVGHHTSVRSIPFPLRY 211
           |||:|||||||||:|||:||::::|:|  :      | :||||||||| | | :||||||
Qy     121 GCHTQYMANMGSVASLALAIVVKGKD--S------S-KLWGLVVGHHCSPRYVPFPLRY 170


RESULT   14
ENTRY            FKMUC      #type complete
TITLE            phytochrome C - Arabidopsis thaliana
ORGANISM         #formal_name Arabidopsis thaliana #common_name mouse-ear
                   cress
DATE             30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change
                   20-Feb-1998
ACCESSIONS       C33473; S07717
REFERENCE        A33473
   #authors      Sharrock, R.A.; Quail, P.H.
   #journal      Genes Dev. (1989) 3:1745-1757
   #title        Novel phytochrome sequences in Arabidopsis thaliana:
                   structure, evolution, and differential expression of a
                   plant regulatory photoreceptor family.
   #cross-references MUID:90108670
   #accession    C33473
      ##molecule_type mRNA
      ##residues      1-1111 ##label SHA
      ##cross-references EMBL:X17343; NID:g16424; PID:g16425
GENETICS
   #gene         phyC
CLASSIFICATION   #superfamily phytochrome; phytochrome homology
KEYWORDS         dimer; photoreceptor; phytochromobilin; transcription
                   regulation
FEATURE
   62-573            #domain phytochrome homology #label PHYT\
   856-1111          #domain signal transduction #label STD\
   318               #binding_site phytochromobilin (Cys) (covalent) #status
                       predicted
SUMMARY          #length 1111  #molecular-weight 123721  #checksum 3846

  Query Match            63.9%;  Score 931;  DB 1;  Length 1111;
  Best Local Similarity  62.6%;  Pred. No. 5.76e-174;
  Matches   129;  Conservative   36;  Mismatches  31;  Indels  10;  Gaps   3;

Db     197 KLAAKSISRLQALPSGNMLLLCDALVKEVSELTGYDRVMVYKFHEDGHGEVIAECCREDM 256
           |||:::|||||:||:|::  |||::| :|  |||||||||| |||| ||||:::|  | |:
Qy       1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL 60

Db     257 EPYLGLHYSATDIPQASRFLFMRNKVRMICDCSAVPVKVVQDKSLSQPISLSGSTLRAPH 316
           ||||||||:|||||||:||||::|:|||||||:| ||||||   | :|: |  |||||||
Qy      61 EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120

Db     317 GCHAQYMSNMGSVASLVMSVTINGSDSDEMNRDLQTGRHLWGLVVCHHASPRFVPFPLRY 376
           |||:|||:|||||||| ::: ::|       :|  ::: |||||| || |||:|||||||
Qy     121 GCHTQYMANMGSVASLALAIVVKG-------KD--SSK-LWGLVVGHHCSPRYVPFPLRY 170

Db     377 ACEFLTQVFGVQINKEAESAVLLKEK 402
           ||||| | ||:|: :| : |  | ||
Qy     171 ACEFLMQAFGLQLQMELQLASQLAEK 196
```

```
RESULT   15
ENTRY            FKPUZ      #type complete
TITLE            phytochrome - zucchini
ORGANISM         #formal_name Cucurbita pepo var. melopepo #common_name
                   zucchini
DATE             30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change
                   20-Feb-1998
ACCESSIONS       S00099
REFERENCE        S00099
   #authors      Sharrock, R.A.; Lissemore, J.L.; Quail, P.H.
   #journal      Gene (1986) 47:287-295
   #title        Nucleotide and amino acid sequence of a Cucurbita phytochrome
                   cDNA clone: identification of conserved features by
                   comparison with Avena phytochrome.
   #cross-references MUID:87163500
   #accession    S00099
      ##molecule_type mRNA
      ##residues      1-1124 ##label SHA
      ##cross-references EMBL:M15265; NID:g167500; PID:g167501
CLASSIFICATION   #superfamily phytochrome; phytochrome homology
KEYWORDS         homodimer; photoreceptor; phytochromobilin; transcription
                   regulation
FEATURE
   67-581             #domain phytochrome homology #label PHYT\
   867-1124           #domain signal transduction #label STD\
   323                #binding_site phytochromobilin (Cys) (covalent) #status
                        predicted
SUMMARY          #length 1124  #molecular-weight 125081  #checksum 3834

  Query Match           60.8%;  Score 886;  DB 1;  Length 1124;
  Best Local Similarity  60.6%;  Pred. No. 6.21e-164;
  Matches   126;  Conservative   37;  Mismatches  33;  Indels  12;  Gaps   5;

Db    202 KLAAKAITRLQSLPSGSMARLCDTMVQEVFELTGYDRVMAYKFHDDDHGEVISEVAKPGL 261
          ||| :||:|||||||:| :: ||||:|::|  |||||||| | ||:|||||||: :: |
Qy      1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL 60

Db    262 QPYLGLHYPATDIPQAARFLFMKNKVRMIVDCRAKHLKVLQDEKLQFDLTLCGSTLRAPH 321
          :|||||||||||||||||||: |:|||| || |  :||:| | |   | |  |||||||
Qy     61 EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120

Db    322 SCHLQYMENMNSIASLVMAVVVNEGDEENEGPALQQQKRKRLWGLVVCHNSSPRFVPFPL 381
          :|| ||| || |:||| :|:||: |   ::: :      | |||||| |: |||:|||||
Qy    121 GCHTQYMANMGSVASLALAIVVK-G---KDS-S------K-LWGLVVGHHCSPRYVPFPL 168

Db    382 RYACEFLAQVFAIHVNKELELENQIIEK 409
          ||||||| | |:::: :||:| :|: ||
Qy    169 RYACEFLMQAFGLQLQMELQLASQLAEK 196


Search completed: Mon Sep 13 14:25:14 1999
Job time : 19 secs.
```

****

MPSRCH (TM)

****

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Sep 13 14:23:31 1999; MasPar time 7.13 Seconds
777.471 Million cell updates/sec

Tabular output not generated.

Title: >US-09-272-809-9
Description: (1-196) from US09272809.pep
Perfect Score: 1458
Sequence: 1 KLAVRAISRLQSLPGGDIGA.....QAFGLQLQMELQLASQLAEK 196

Scoring table: PAM 150
Gap 11

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot37
1:swissprot

Statistics: Mean 45.285; Variance 72.284; scale 0.626

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1458	100.0	1112	1	PHYE_ARATH	PHYTOCHROME E.	0.00e+00
2	1311	89.9	1115	1	PHYE_PHANI	PHYTOCHROME E.	2.57e-301
3	1143	78.4	1132	1	PHYB_TOBAC	PHYTOCHROME B.	3.10e-257
4	1138	78.1	1131	1	PHY_PINSY	PHYTOCHROME.	6.31e-256
5	1070	73.4	1172	1	PHYB_ARATH	PHYTOCHROME B.	3.71e-238
6	1066	73.1	1171	1	PHYB_ORYSA	PHYTOCHROME B.	4.11e-237
7	1058	72.6	1156	1	PHYB_SOYBN	PHYTOCHROME B.	5.02e-235
8	1035	71.0	1117	1	PHY_ADICA	PHYTOCHROME.	4.99e-229
9	1032	70.8	1164	1	PHYD_ARATH	PHYTOCHROME D.	3.02e-228
10	1030	70.6	1121	1	PHY2_CERPU	PHYTOCHROME 2.	1.00e-227
11	1027	70.4	1129	1	PHYB_SOLTU	PHYTOCHROME B.	6.06e-227
12	1016	69.7	1132	1	PHY1_PHYPA	PHYTOCHROME 1.	4.44e-224
13	996	68.3	1136	1	PHY_PICAB	PHYTOCHROME.	7.13e-219
14	986	67.6	1307	1	PHY1_CERPU	PHYTOCHROME / PROTEIN	2.85e-216
15	977	67.0	1124	1	PHY_MOUSC	PHYTOCHROME.	6.23e-214
16	969	66.5	1134	1	PHY1_SELMA	PHYTOCHROME 1.	7.47e-212
17	931	63.9	1111	1	PHYC_ARATH	PHYTOCHROME C.	5.47e-202
18	893	61.2	1124	1	PHY1_TOBAC	PHYTOCHROME A1.	3.82e-192
19	886	60.8	1124	1	PHYA_CUCPE	PHYTOCHROME A.	2.47e-190
20	883	60.6	1123	1	PHYA_SOLTU	PHYTOCHROME A.	1.48e-189
21	873	59.9	1125	1	PHYA_POPTM	PHYTOCHROME A.	5.69e-187
22	865	59.3	1122	1	PHYA_ARATH	PHYTOCHROME A.	6.65e-185
23	864	59.3	1124	1	PHYA_PEA	PHYTOCHROME A.	1.21e-184
24	864	59.3	1124	1	PHYA_LATSA	PHYTOCHROME TYPE A.	1.21e-184
25	865	59.3	1129	1	PHYA_PETCR	PHYTOCHROME A.	6.65e-185
26	860	59.0	1131	1	PHYA_SOYBN	PHYTOCHROME A.	1.30e-183
27	845	58.0	494	1	PHY5_AVESA	PHYTOCHROME A TYPE 5 (	9.70e-180
28	845	58.0	1128	1	PHY4_AVESA	PHYTOCHROME A TYPE 4 (	9.70e-180
29	837	57.4	1128	1	PHY3_AVESA	PHYTOCHROME A TYPE 3 (	1.12e-177
30	836	57.3	1128	1	PHYA_ORYSA	PHYTOCHROME A.	2.03e-177
31	831	57.0	1131	1	PHYA_MAIZE	PHYTOCHROME A.	3.96e-176
32	552	37.9	748	1	Y473_SYNY3	HYPOTHETICAL 84.2 KD P	4.55e-105
33	105	7.2	422	1	YURO_BACSU	HYPOTHETICAL ABC TRANS	5.51e-03
34	105	7.2	715	1	Y07J_MYCTU	HYPOTHETICAL 78.2 KD P	5.51e-03
35	104	7.1	407	1	IHBB_HUMAN	INHIBIN BETA B CHAIN P	7.98e-03
36	102	7.0	255	1	IHBB_MOUSE	INHIBIN BETA B CHAIN P	1.66e-02
37	100	6.9	386	1	CYB_HANWI	CYTOCHROME B (EC 1.10.	3.43e-02
38	101	6.9	874	1	DP3A_MYCGE	DNA POLYMERASE III, AL	2.39e-02
39	96	6.6	360	1	LEU3_PSEAE	3-ISOPROPYLMALATE DEHY	1.42e-01
40	91	6.2	349	1	IHBB_PIG	INHIBIN BETA B CHAIN P	7.85e-01
41	91	6.2	379	1	HUPD_AZOCH	HYDROGENASE EXPRESSION	7.85e-01
42	90	6.2	485	1	SAHH_MESCR	ADENOSYLHOMOCYSTEINASE	1.10e+00
43	89	6.1	242	1	RSTA_ECOLI	TRANSCRIPTIONAL REGULA	1.52e+00
44	89	6.1	502	1	SKS1_YEAST	SERINE/THREONINE-PROTE	1.52e+00
45	88	6.0	810	1	YP07_YEAST	HYPOTHETICAL 89.8 KD P	2.11e+00

ALIGNMENTS

```
RESULT    1
ID   PHYE_ARATH     STANDARD;      PRT;  1112 AA.
AC   P42498;
DT   01-NOV-1995 (REL. 32, CREATED)
DT   01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT   01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE   PHYTOCHROME E.
GN   PHYE.
OS   ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
OC   EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC   EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
OC   CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. LANDSBERG ERECTA;
RX   MEDLINE; 94325466.
RA   CLACK T., MATHEWS S., SHARROCK R.A.;
RT   "The phytochrome apoprotein family in Arabidopsis is encoded by five
RT   genes: the sequences and expression of PHYD and PHYE.";
RL   PLANT MOL. BIOL. 25:413-427(1994).
CC   -!- FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT
CC       ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS
CC       MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PFR FORM THAT
CC       ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN
CC       PFR INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS
CC       RECONVERSION OF PFR TO PR CANCELS THE INDUCTION OF THOSE
CC       RESPONSES. PFR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR
CC       GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-
CC       BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN,
CC       PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS
CC       THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION.
CC   -!- SUBUNIT: HOMODIMER.
CC   -!- PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X76610; G452817; -.
DR   PROSITE; PS00245; PHYTOCHROME_1; 1.
DR   PROSITE; PS50046; PHYTOCHROME_2; 1.
DR   PFAM; PF00360; phytochrome; 1.
DR   PFAM; PF00512; signal; 1.
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DR   PFAM; PF00989; PAS; 2.
DR   MENDEL; 7190; ARAth;PhyE;1.
KW   TRANSCRIPTION REGULATION; PHOTORECEPTOR; PHYTOCHROME; CHROMOPHORE;
KW   MULTIGENE FAMILY.
FT   BINDING     322    322       CHROMOPHORE (BY SIMILARITY).
SQ   SEQUENCE   1112 AA;  122587 MW;  C9D173CE CRC32;

  Query Match          100.0%;  Score 1458;  DB 1;  Length 1112;
  Best Local Similarity 100.0%;  Pred. No. 0.00e+00;
  Matches   196;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db     201 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL 260
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy       1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL 60

Db     261 EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 320
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy      61 EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120

Db     321 GCHTQYMANMGSVASLALAIVVKGKDSSKLWGLVVGHHCSPRYVPFPLRYACEFLMQAFG 380
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     121 GCHTQYMANMGSVASLALAIVVKGKDSSKLWGLVVGHHCSPRYVPFPLRYACEFLMQAFG 180

Db     381 LQLQMELQLASQLAEK 396
         ||||||||||||||||
Qy     181 LQLQMELQLASQLAEK 196


RESULT    2
ID   PHYE_PHANI     STANDARD;      PRT;  1115 AA.
AC   P55004;
DT   01-OCT-1996 (REL. 34, CREATED)
DT   01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   PHYTOCHROME E.
GN   PHYE.
OS   PHARBITIS NIL (VIOLET) (JAPANESE MORNING GLORY).
OC   EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC   EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
OC   ASTERIDAE; SOLANANAE; SOLANALES; CONVOLVULACEAE; IPOMOEA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=SEEDLING COTYLEDON;
RA   ZHENG C.C., O'NEILL S.D.;
RL   SUBMITTED (JAN-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
CC   -!- FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT
CC       ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS
CC       MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PFR FORM THAT
CC       ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN
CC       PFR INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS
CC       RECONVERSION OF PFR TO PR CANCELS THE INDUCTION OF THOSE
CC       RESPONSES. PFR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR
CC       GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-
CC       BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN,
CC       PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS
CC       THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION.
CC   -!- SUBUNIT: HOMODIMER.
CC   -!- PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U39787; G1145714; -.
DR   PROSITE; PS00245; PHYTOCHROME_1; 1.
DR   PROSITE; PS50046; PHYTOCHROME_2; 1.
DR   PFAM; PF00360; phytochrome; 1.
DR   PFAM; PF00512; signal; 1.
DR   PFAM; PF00989; PAS; 2.
KW   TRANSCRIPTION REGULATION; PHOTORECEPTOR; PHYTOCHROME; CHROMOPHORE.
FT   BINDING     318    318       CHROMOPHORE (BY SIMILARITY).
SQ   SEQUENCE   1115 AA;  124328 MW;  09FCF0BA CRC32;

  Query Match          89.9%;  Score 1311;  DB 1;  Length 1115;
  Best Local Similarity 87.2%;  Pred. No. 2.57e-301;
  Matches   171;  Conservative   14;  Mismatches  11;  Indels   0;  Gaps   0;

Db     197 KLAVRAISRLQSLPGGDIGTLCDTVVEDVQKLTGYDRVMVYKFHDDSHGEVVSEIRRSDL 256
         |||||||||||||||||||:||||||||||:|||||||||| ||:| ||||||||||||
Qy       1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL 60

Db     257 EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNAQPVKVLQCEELKQPLCLVNSTLRSPH 316
         |||||||||||||||||||||||||||||||| ||||:| ||||:||||||||:||
Qy      61 EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120

Db     317 GCHTKYMANMGSIASLVMAVVINSSESMKLWGLVVCHHTSPRYVPFPLRYACEFLMQAFS 376
         |||| ||||||||||| :|:|::: :| ||||||| || ||||||||||||||||||||:
Qy     121 GCHTQYMANMGSVASLALAIVVKGKDSSKLWGLVVGHHCSPRYVPFPLRYACEFLMQAFG 180

Db     377 LQLYMELQLASQLAEK 392
         ||| ||||||||||||
Qy     181 LQLQMELQLASQLAEK 196


RESULT    3
ID   PHYB_TOBAC     STANDARD;      PRT;  1132 AA.
AC   P29130;
DT   01-DEC-1992 (REL. 24, CREATED)
DT   01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DT   01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE   PHYTOCHROME B.
GN   PHYB.
OS   NICOTIANA TABACUM (COMMON TOBACCO).
OC   EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC   EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
OC   ASTERIDAE; SOLANANAE; SOLANALES; SOLANACEAE; NICOTIANA.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   KERN R., GASCH A., DEAK M., KAY S.A., CHUA N.H.;
RL   SUBMITTED (XXX-1993) TO EMBL/GENBANK/DDBJ DATA BANKS.
RN   [2]
RP   SEQUENCE OF 457-1132 FROM N.A.
RX   MEDLINE; 92361250.
RA   LOPEZ-JUEZ E., NAGATANI A., TOMIZAWA K.I., DEAK M., KERN R.,
RA   KENDRICK R.E., FURUYA M.;
RT   "The cucumber long hypocotyl mutant lacks a light-stable PHYB-like
RT   phytochrome.";
RL   PLANT CELL 4:241-251(1992).
CC   -!- FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT
CC       ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS
CC       MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PFR FORM THAT
CC       ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN
CC       PFR INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS
CC       RECONVERSION OF PFR TO PR CANCELS THE INDUCTION OF THOSE
CC       RESPONSES. PFR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR
CC       GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-
CC       BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN,
CC       PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS
CC       THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION.
CC   -!- SUBUNIT: HOMODIMER.
CC   -!- PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.
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CC   ---------------------------------------------------------------------
DR   EMBL; L10114; G295346; -.
DR   EMBL; M65023; G170287; -.
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DR   PROSITE; PS00245; PHYTOCHROME_1; 1.
DR   PROSITE; PS50046; PHYTOCHROME_2; 1.
DR   PFAM; PF00360; phytochrome; 1.
DR   PFAM; PF00512; signal; 1.
DR   PFAM; PF00989; PAS; 2.
DR   MENDEL; 1321; NICta;PhyB;1.
KW   TRANSCRIPTION REGULATION; PHOTORECEPTOR; PHYTOCHROME; CHROMOPHORE;
KW   MULTIGENE FAMILY.
FT   BINDING     336    336       CHROMOPHORE (BY SIMILARITY).
FT   CONFLICT    507    507       L -> S (IN REF. 2).
FT   CONFLICT    586    586       L -> LQ (IN REF. 2).
SQ   SEQUENCE   1132 AA;  125809 MW;  6CD35D63 CRC32;

  Query Match           78.4%;  Score 1143;  DB 1;  Length 1132;
  Best Local Similarity  77.0%;  Pred. No. 3.10e-257;
  Matches   157;  Conservative   25;  Mismatches  14;  Indels   8;  Gaps   2;

Db    215 KLAVRAISHLQSLPGGDVKLLCDTVVESVRELTGYDRVMVYKFHEDEHGEVVAESKIPDL 274
          ||||||||:||||||||:  ||||||| |: |||||||||| ||||:|||||:| : :||
Qy      1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL 60

Db    275 EPYIGLHYPATDIPQASRFLFKQNRVRMIVDCHATPVRVVQDESLMQPLCLVGSTLRAPH 334
          |||:|||||||||||:|||||||||||| ||:||||:||| | |::||||| |||||||
Qy     61 EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120

Db    335 GCHAQYMANMGSIASLTLAVIINGNDEEAVGGRSSMRLWGLVVGHHTSARCIPFPLRYAC 394
          |||:|||||||||:|||:||::::|:|      || :|||||||| |:| :|||||||
Qy    121 GCHTQYMANMGSVASLALAIVVKGKD-------SS-KLWGLVVGHHCSPRYVPFPLRYAC 172

Db    395 EFLMQAFGLQLNMELQLASQLSEK 418
          |||||||||| |||||||||:||
Qy    173 EFLMQAFGLQLQMELQLASQLAEK 196


RESULT    4
ID   PHY_PINSY      STANDARD;      PRT;  1131 AA.
AC   Q41046;
DT   01-NOV-1997 (REL. 35, CREATED)
DT   01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   PHYTOCHROME.
OS   PINUS SYLVESTRIS (SCOTS PINE).
OC   EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC   EUPHYLLOPHYTES; SPERMATOPHYTA; CONIFEROPSIDA; CONIFERALES; PINACEAE;
OC   PINUS.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=PSA 5.1;
RA   WIEGMANN-EIRUND C.M., KOLUKISAOGLU H.U.;
RL   SUBMITTED (MAR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
CC   -!- FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT
CC       ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS
CC       MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PFR FORM THAT
CC       ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN
CC       PFR INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS
CC       RECONVERSION OF PFR TO PR CANCELS THE INDUCTION OF THOSE
CC       RESPONSES. PFR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR
CC       GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-
CC       BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN,
CC       PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS
CC       THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION.
CC   -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC   -!- PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X96738; E229831; -.
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DR   PROSITE; PS00245; PHYTOCHROME_1; 1.
DR   PROSITE; PS50046; PHYTOCHROME_2; 1.
DR   PFAM; PF00360; phytochrome; 1.
DR   PFAM; PF00512; signal; 1.
DR   PFAM; PF00989; PAS; 2.
KW   TRANSCRIPTION REGULATION; PHOTORECEPTOR; PHYTOCHROME; CHROMOPHORE.
FT   BINDING     332    332       CHROMOPHORE (BY SIMILARITY).
SQ   SEQUENCE   1131 AA;  126254 MW;  DEFCE259 CRC32;

  Query Match           78.1%;  Score 1138;  DB 1;  Length 1131;
  Best Local Similarity  78.5%;  Pred. No. 6.31e-256;
  Matches   161;  Conservative   21;  Mismatches  14;  Indels   9;  Gaps   3;

Db    211 KLAVRAISRLQSLPCGDVGLLCDTVVENVRELTGYDRVMVYKFHEDEHGEVVAEIRRSDL 270
          |||||||||||||| ||:| |||||||:|: |||||||||| ||||:||||||||||||
Qy      1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL 60

Db    271 EPYLGLHYPATDIPQASRFLFMQNRVRMICDCMATPVKVIQSEELMQPLCLVGSTPSAPH 330
          |||||||||||||||:||||:|||||||||| ||||||:|||||::||||| ||  |||
Qy     61 EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120

Db    331 GCHAQYMANMGSIRSLLMAVIINGNDDEGGGSGRNSMKLWGLVVCHHTSPRAVPFPLRYA 390
          |||:|||||||: || :|::::|:|     |   | ||||||| || ||| ||||||||
Qy    121 GCHTQYMANMGSVASLALAIVVKGKD-----S---S-KLWGLVVGHHCSPRYVPFPLRYA 171

Db    391 CEFLMQALGLQLNMELQLAAQLTEK 415
          |||||||:|||| ||||||:||:||
Qy    172 CEFLMQAFGLQLQMELQLASQLAEK 196


RESULT    5
ID   PHYB_ARATH     STANDARD;      PRT;  1172 AA.
AC   P14713;
DT   01-APR-1990 (REL. 14, CREATED)
DT   01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
DT   01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE   PHYTOCHROME B.
GN   PHYB OR HY3.
OS   ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
OC   EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC   EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
OC   CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. COLUMBIA;
RX   MEDLINE; 90108670.
RA   SHARROCK R.A., QUAIL P.H.;
RT   "Novel phytochrome sequences in Arabidopsis thaliana: structure,
RT   evolution, and differential expression of a plant regulatory
RT   photoreceptor family.";
RL   GENES DEV. 3:1745-1757(1989).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. LANDSBERG ERECTA;
RX   MEDLINE; 93200802.
RA   REED J.W., NAGPAL P., POOLE D.S., FURUYA M., CHORY J.;
RT   "Mutations in the gene for the red/far-red light receptor phytochrome
RT   B alter cell elongation and physiological responses throughout
RT   Arabidopsis development.";
RL   PLANT CELL 5:147-157(1993).
CC   -!- FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT
CC       ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS
CC       MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PFR FORM THAT
CC       ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN
CC       PFR INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS
CC       RECONVERSION OF PFR TO PR CANCELS THE INDUCTION OF THOSE
CC       RESPONSES. PFR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR
CC       GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-
CC       BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN,
CC       PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS
CC       THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION.
CC   -!- SUBUNIT: HOMODIMER.
CC   -!- PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.
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CC   ----------------------------------------------------------------------
DR   EMBL; X17342; G16423; -.
DR   EMBL; L09262; -; NOT_ANNOTATED_CDS.
DR   PIR; S07718; FKMUB.
DR   PIR; JQ2141; JQ2141.
DR   PROSITE; PS00245; PHYTOCHROME_1; 1.
DR   PROSITE; PS50046; PHYTOCHROME_2; 1.
DR   PFAM; PF00360; phytochrome; 1.
DR   PFAM; PF00512; signal; 1.
DR   PFAM; PF00989; PAS; 2.
DR   MENDEL; 1310; ARAth;PhyB;1.
KW   TRANSCRIPTION REGULATION; PHOTORECEPTOR; PHYTOCHROME; CHROMOPHORE;
KW   MULTIGENE FAMILY.
FT   DOMAIN        3     25       GLY/SER-RICH.
FT   BINDING     357    357       CHROMOPHORE.
SQ   SEQUENCE   1172 AA;  129331 MW;  2FC0BA87 CRC32;

  Query Match           73.4%;  Score 1070;  DB 1;  Length 1172;
  Best Local Similarity  73.9%;  Pred. No. 3.71e-238;
  Matches   153;  Conservative   25;  Mismatches  18;  Indels  11;  Gaps   3;

Db    236 KLAVRAISQLQALPGGDIKLLCDTVVESVRDLTGYDRVMVYKFHEDEHGEVVAESKRDDL 295
            |||||||||:||:||||||  ||||||| |: |||||||||| ||||:|||||:| :| ||
Qy      1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL 60

Db    296 EPYIGLHYPATDIPQASRFLFKQNRVRMIVDCNATPVLVVQDDRLTQSMCLVGSTLRAPH 355
            |||:||||||||||:|||||||||||| |||||| ||| : | :::||| |||||||
Qy     61 EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120

Db    356 GCHSQYMANMGSIASLAMAVIINGNEDDGSNVASGRSSMRLWGLVVCHHTSSRCIPFPLR 415
            |||:|||||||:||||:|::::|:  |       || :|||||| || |:| :|||||
Qy    121 GCHTQYMANMGSVASLALAIVVKGK--D--------SS-KLWGLVVGHHCSPRYVPFPLR 169

Db    416 YACEFLMQAFGLQLNMELQLALQMSEK 442
            |||||||||||||| |||||| |::||
Qy    170 YACEFLMQAFGLQLQMELQLASQLAEK 196


RESULT    6
ID   PHYB_ORYSA     STANDARD;      PRT;  1171 AA.
AC   P25764;
DT   01-MAY-1992 (REL. 22, CREATED)
DT   01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
DT   01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE   PHYTOCHROME B.
GN   PHYB OR PHYB1.
OS   ORYZA SATIVA (RICE).
OC   EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC   EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES;
OC   POACEAE; ORYZA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. INDICA-IR36; TISSUE=SEEDLING SHOOT;
RX   MEDLINE; 91172131.
RA   DEHESH K., TEPPERMAN J., CHRISTENSEN A.H., QUAIL P.H.;
RT   "phyB is evolutionarily conserved and constitutively expressed in
RT   rice seedling shoots.";
RL   MOL. GEN. GENET. 225:305-313(1991).
CC   -!- FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT
CC       ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS
CC       MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PFR FORM THAT
CC       ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN
CC       PFR INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS
CC       RECONVERSION OF PFR TO PR CANCELS THE INDUCTION OF THOSE
CC       RESPONSES. PFR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR
CC       GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-
CC       BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN,
CC       PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS
CC       THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION.
CC   -!- SUBUNIT: HOMODIMER.
CC   -!- PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.
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CC   ----------------------------------------------------------------------
DR   EMBL; X57563; G20290; ALT_SEQ.
DR   PIR; S14065; S14065.
DR   PROSITE; PS00245; PHYTOCHROME_1; 1.
DR   PROSITE; PS50046; PHYTOCHROME_2; 1.
DR   PFAM; PF00360; phytochrome; 1.
DR   PFAM; PF00512; signal; 1.
DR   PFAM; PF00989; PAS; 2.
DR   MENDEL; 1319; ORYsa;PhyB;1.
KW   TRANSCRIPTION REGULATION; PHOTORECEPTOR; PHYTOCHROME; CHROMOPHORE;
KW   MULTIGENE FAMILY.
FT   DOMAIN       39     51       POLY-GLY.
FT   BINDING     364    364       CHROMOPHORE (BY SIMILARITY).
SQ   SEQUENCE   1171 AA;  128384 MW;  1FC77209 CRC32;

  Query Match           73.1%;  Score 1066;  DB 1;  Length 1171;
  Best Local Similarity  72.7%;  Pred. No. 4.11e-237;
  Matches   152;  Conservative   23;  Mismatches  21;  Indels  13;  Gaps   4;

Db    243 KLVVRAISRLQALPGGDVKLLCDTVVEHVRELTGYDRVMVYRFHEDEHGEVVAESRRSNL 302
            || |||||||:||||:  ||||||| |: |||||||||:||||:|||||:| |||:|
Qy      1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL 60

Db    303 EPYIGLHYPATDIPQASRFLFRQNRVRMIADCHAAPVRVIQDPALTQPLCLVGSTLRSPH 362
            |||:|||||||||||:||||:||||||| ||:|:||:|:|   | :|||| ||||:||
Qy     61 EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120

Db    363 GCHGQYMANMGSIASLVMAVIISSGGDDDHNIARGSIPSAMKLWGLVVCHHTSPRCIPFP 422
            ||| |||||||:||| :|:::   | |       |  |  ||||||| || ||| :|||
Qy    121 GCHTQYMANMGSVASLALAIVVK--GKD-------S--S--KLWGLVVGHHCSPRYVPFP 167

Db    423 LRYACEFLMQAFGLQLNMELQLAHQLSEK 451
            ||||||||||||||| |||||| ||:||
Qy    168 LRYACEFLMQAFGLQLQMELQLASQLAEK 196


RESULT    7
ID   PHYB_SOYBN     STANDARD;      PRT;  1156 AA.
AC   P42499;
DT   01-NOV-1995 (REL. 32, CREATED)
DT   01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT   15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
DE   PHYTOCHROME B.
GN   PHYB.
OS   GLYCINE MAX (SOYBEAN).
OC   EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC   EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
OC   FABALES; FABACEAE; PAPILIONOIDEAE; GLYCINE.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. PALDAL; TISSUE=ETIOLATED LEAF;
RA   HAHN T.R., WOO T.W., SEO H.S., CHOI Y.D.;
RL   SUBMITTED (XXX-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.
CC   -!- FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT
CC       ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS
CC       MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PFR FORM THAT
CC       ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN
CC       PFR INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS
CC       RECONVERSION OF PFR TO PR CANCELS THE INDUCTION OF THOSE
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CC       RESPONSES. PFR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR
CC       GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-
CC       BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN,
CC       PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS
CC       THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION.
CC   -!- SUBUNIT: HOMODIMER.
CC   -!- PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.
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CC   ---------------------------------------------------------------------
DR   EMBL; L34843; G516103; -.
DR   PROSITE; PS00245; PHYTOCHROME_1; 1.
DR   PROSITE; PS50046; PHYTOCHROME_2; 1.
DR   PFAM; PF00360; phytochrome; 2.
DR   PFAM; PF00512; signal; 1.
DR   PFAM; PF00989; PAS; 2.
DR   MENDEL; 8366; GLYma;PhyB;1.
KW   TRANSCRIPTION REGULATION; PHOTORECEPTOR; PHYTOCHROME; CHROMOPHORE;
KW   MULTIGENE FAMILY.
FT   BINDING     358    358       CHROMOPHORE (BY SIMILARITY).
SQ   SEQUENCE   1156 AA;  129085 MW;  1A96C07F CRC32;

  Query Match           72.6%;  Score 1058;  DB 1;  Length 1156;
  Best Local Similarity  73.1%;  Pred. No. 5.02e-235;
  Matches   147;  Conservative   27;  Mismatches  19;  Indels   8;  Gaps   2;

Db    240 VRAISQLQSLPSADVKLLCDTVVESVRELTGYDRVMVYKFHEDEHGEVVSESKRPDLEPY 299
          |||||:|||||::|:  ||||||| |: |||||||||| ||||:||||||| :|:|||||
Qy      4 VRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDLEPY 63

Db    300 IGLHYPATDIPQASRFLFKQNRVRMIVDCHASAVRVVQDEALVQPLCLVGSTLGAPHGCH 359
          :|||||||||||:|||||||||||| ||:|::|:||| | | :||||| ||| ||||||
Qy     64 LGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPHGCH 123

Db    360 AQYMANMGSIASLVMAVIINGNDEEGVGGRSSMRLWGLVVCHHTSARCIPFPLRYACEFL 419
          :|||||||:||| :|::::|:|       || :|||||| || |:| :|||||||||||
Qy    124 TQYMANMGSVASLALAIVVKGKD-------SS-KLWGLVVGHHCSPRYVPFPLRYACEFL 175

Db    420 MQAFGLQLNMELQLAAQSLEK 440
          |||||||| ||||||:|  ||
Qy    176 MQAFGLQLQMELQLASQLAEK 196


RESULT    8
ID   PHY_ADICA      STANDARD;      PRT;  1117 AA.
AC   P42496;
DT   01-NOV-1995 (REL. 32, CREATED)
DT   01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT   01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE   PHYTOCHROME.
OS   ADIANTUM CAPILLUS-VENERIS (FERN).
OC   EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC   EUPHYLLOPHYTES; FILICOPHYTA; FILICOPSIDA; FILICALES; ADIANTACEAE;
OC   ADIANTUM.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   OKAMOTO H., HIRANO Y., ABE H., TOMIZAWA K.I., FURUYA M., WADA M.;
RT   "The deduced amino sequence of phytochrome from Adiantum includes
RT   consensus motifs present in phytochrome B from seed plants.";
RL   PLANT CELL PHYSIOL. 34:1329-1334(1993).
CC   -!- FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT
CC       ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS
CC       MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PFR FORM THAT
CC       ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN
CC       PFR INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS
CC       RECONVERSION OF PFR TO PR CANCELS THE INDUCTION OF THOSE
CC       RESPONSES. PFR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR
CC       GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-
CC       BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN,
CC       PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS
CC       THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION.
CC   -!- SUBUNIT: HOMODIMER.
CC   -!- PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.
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CC   ---------------------------------------------------------------------
DR   EMBL; D13519; D1003241; -.
DR   PROSITE; PS00245; PHYTOCHROME_1; 1.
DR   PROSITE; PS50046; PHYTOCHROME_2; 1.
DR   PFAM; PF00360; phytochrome; 1.
DR   PFAM; PF00512; signal; 1.
DR   PFAM; PF00989; PAS; 2.
KW   TRANSCRIPTION REGULATION; PHOTORECEPTOR; PHYTOCHROME; CHROMOPHORE.
FT   BINDING     316    316       CHROMOPHORE (BY SIMILARITY).
SQ   SEQUENCE   1117 AA;  123734 MW;  CCE19DC2 CRC32;

  Query Match           71.0%;  Score 1035;  DB 1;  Length 1117;
  Best Local Similarity  69.3%;  Pred. No. 4.99e-229;
  Matches   142;  Conservative   28;  Mismatches  26;  Indels   9;  Gaps   3;

Db    195 KLAAKAIARLQSLPGGDIGLLCDSVVEEVHELTGFDRVMAYKFHEDEHGEVVAEIRRTDL 254
          ||| :||:|||||||||| |||:|||:|: |||:|||| | ||||:|||||:||||:|| 
Qy      1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL 60

Db    255 EPYIGLHYPATDIPQAARFLFMKNRVRMICDCRLPPVKLIQDKTLSQPMSLTGSTLRAPH 314
          |||:|||||||||||||||: |||||||||   |||::|   | :|: |  |||||||
Qy     61 EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120

Db    315 GCHTQYMANMNSISSLVMAVIVNDSDDDSAGHSSQGIKLWGLVVCHHTSPRYVPFPVRSA 374
          |||||||||| |::|| :|::|: : |     ||   ||||||| || |||||||:| |
Qy    121 GCHTQYMANMGSVASLALAIVVK-GKD-----SS---KLWGLVVGHHCSPRYVPFPLRYA 171

Db    375 CEFLMQVFSLQLNMEVGMAAQVREK 399
          |||||| |:||| ||: :|:|: ||
Qy    172 CEFLMQAFGLQLQMELQLASQLAEK 196


RESULT    9
ID   PHYD_ARATH     STANDARD;      PRT;  1164 AA.
AC   P42497;
DT   01-NOV-1995 (REL. 32, CREATED)
DT   01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT   01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE   PHYTOCHROME D.
GN   PHYD.
OS   ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
OC   EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC   EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
OC   CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. LANDSBERG ERECTA;
RX   MEDLINE; 94325466.
RA   CLACK T., MATHEWS S., SHARROCK R.A.;
RT   "The phytochrome apoprotein family in Arabidopsis is encoded by five
RT   genes: the sequences and expression of PHYD and PHYE.";
RL   PLANT MOL. BIOL. 25:413-427(1994).
CC   -!- FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT
CC       ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS
CC       MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PFR FORM THAT
CC       ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN
CC       PFR INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS
CC       RECONVERSION OF PFR TO PR CANCELS THE INDUCTION OF THOSE
CC       RESPONSES. PFR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR
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CC       GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-
CC       BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN,
CC       PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS
CC       THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION.
CC   -!- SUBUNIT: HOMODIMER.
CC   -!- PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.
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CC   ---------------------------------------------------------------------
DR   EMBL; X76609; G452814; -.
DR   PROSITE; PS00245; PHYTOCHROME_1; 1.
DR   PROSITE; PS50046; PHYTOCHROME_2; 1.
DR   PFAM; PF00360; phytochrome; 1.
DR   PFAM; PF00512; signal; 1.
DR   PFAM; PF00989; PAS; 2.
DR   MENDEL; 7189; ARAth;PhyD;1.
KW   TRANSCRIPTION REGULATION; PHOTORECEPTOR; PHYTOCHROME; CHROMOPHORE;
KW   MULTIGENE FAMILY.
FT   BINDING     360    360       CHROMOPHORE (BY SIMILARITY).
SQ   SEQUENCE   1164 AA;  129301 MW;  6BC8A3F1 CRC32;

  Query Match           70.8%;  Score 1032;  DB 1;  Length 1164;
  Best Local Similarity  71.2%;  Pred. No. 3.02e-228;
  Matches   148;  Conservative   30;  Mismatches  18;  Indels  12;  Gaps   4;

Db    239 KLAVRAISHLQSLPSGDIKLLCDTVVESVRDLTGYDRVMVYKFHEDEHGEVVAESKRNDL 298
          |||||||:|||||:|||  ||||||| |: |||||||||| ||||:||||||:| :|:||
Qy      1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL 60

Db    299 EPYIGLHYPATDIPQASRFLFKQNRVRMIVDCYASPVRVVQDDRLTQFICLVGSTLRAPH 358
          |||:|||||||||||||:|||||||||||| || |:||:||| : | : :||| |||||||
Qy     61 EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120

Db    359 GCHAQYMTNMGSIASLAMAVIINGNEEDGNGVNTGGRNSMRLWGLVVCHHTSARCIPFPL 418
          |||:|||:||||:||||:|::::|:  |     :    | :|||||| || |:| :||||
Qy    121 GCHTQYMANMGSVASLALAIVVKGK--D-----S----S-KLWGLVVGHHCSPRYVPFPL 168

Db    419 RYACEFFMQAFGLQLNMELQLALQVSEK 446
          ||||||:|||||||| |||||| |::||
Qy    169 RYACEFLMQAFGLQLQMELQLASQLAEK 196


RESULT   10
ID   PHY2_CERPU     STANDARD;      PRT;  1121 AA.
AC   Q39557;
DT   01-NOV-1997 (REL. 35, CREATED)
DT   01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT   15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE   PHYTOCHROME 2.
GN   PHY2.
OS   CERATODON PURPUREUS (MOSS).
OC   EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; BRYOPSIDA;
OC   BRYIDAE; DICRANALES; DITRICHACEAE; CERATODON.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   LAMPARTER T., MITTMANN F.;
RT   "CERPU;PHY0;2, a 'normal' phytochrome in Ceratodon.";
RL   (IN) PLANT GENE REGISTER PGR96-067.
CC   -!- FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT
CC       ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS
CC       MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PFR FORM THAT
CC       ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN
CC       PFR INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS
CC       RECONVERSION OF PFR TO PR CANCELS THE INDUCTION OF THOSE
CC       RESPONSES. PFR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR
CC       GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-
CC       BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN,
CC       PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS
CC       THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION.
CC   -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC   -!- PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U56698; G1314837; -.
DR   PROSITE; PS00245; PHYTOCHROME_1; 1.
DR   PROSITE; PS50046; PHYTOCHROME_2; 1.
DR   PFAM; PF00360; phytochrome; 1.
DR   PFAM; PF00512; signal; 1.
DR   PFAM; PF00989; PAS; 2.
KW   TRANSCRIPTION REGULATION; PHOTORECEPTOR; PHYTOCHROME; CHROMOPHORE;
KW   MULTIGENE FAMILY.
FT   BINDING     319    319       CHROMOPHORE (BY SIMILARITY).
SQ   SEQUENCE   1121 AA;  124126 MW;  519F6AD4 CRC32;

  Query Match           70.6%;  Score 1030;  DB 1;  Length 1121;
  Best Local Similarity  69.3%;  Pred. No. 1.00e-227;
  Matches   142;  Conservative   31;  Mismatches  23;  Indels   9;  Gaps   3;

Db    198 KLAAKAITRLQALPGGDIGLLCDTVVEEVRELTGYDRVMAYKFHEDEHGEVVAEIRRMDL 257
          ||| :||:|||:||||||| |||||||:|: |||||||| | ||||:|||||:|||| ||
Qy      1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL 60

Db    258 EPYLGLHYPATDIPQASRFLFMKNRVRVIADCCASPVKLIQDPPDIKQPVSLAGSTLRAPH 317
          |||||||||||||||:|||||: ||||:| || |:|||::|  ::|:|: |  |||||||
Qy     61 EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120

Db    318 GCHAQYMGNMGSIASLVMAVIINDNEEDSRGAIQRGRKLWGLVVCHHTSPRTVPFPLRSA 377
          |||:|||:||||:||| :|:::: :  ||  :     ||||||| || ||| ||||||
Qy    121 GCHTQYMANMGSVASLALAIVVKGK--DS--S-----KLWGLVVGHHCSPRYVPFPLRYA 171

Db    378 CEFLMQVFGMQLNMEVELAAQLREK 402
          |||||| ||:|| ||::||:|| ||
Qy    172 CEFLMQAFGLQLQMELQLASQLAEK 196


RESULT   11
ID   PHYB_SOLTU     STANDARD;      PRT;  1129 AA.
AC   P34094;
DT   01-FEB-1994 (REL. 28, CREATED)
DT   01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DT   01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE   PHYTOCHROME B.
GN   PHYB.
OS   SOLANUM TUBEROSUM (POTATO).
OC   EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC   EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
OC   ASTERIDAE; SOLANANAE; SOLANALES; SOLANACEAE; SOLANUM.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 93081720.
RA   HEYER A., GATZ C.;
RT   "Isolation and characterization of a cDNA-clone coding for potato
RT   type B phytochrome.";
RL   PLANT MOL. BIOL. 20:589-600(1992).
CC   -!- FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT
CC       ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS
CC       MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PFR FORM THAT
CC       ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN
CC       PFR INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS
CC       RECONVERSION OF PFR TO PR CANCELS THE INDUCTION OF THOSE
CC       RESPONSES. PFR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR
CC       GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-
CC       BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN,
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CC       PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS
CC       THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION.
CC   -!- SUBUNIT: HOMODIMER.
CC   -!- PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.
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CC   ---------------------------------------------------------------------
DR   EMBL; S51538; G261209; -.
DR   PIR; S28431; S28431.
DR   PROSITE; PS00245; PHYTOCHROME_1; 1.
DR   PROSITE; PS50046; PHYTOCHROME_2; 1.
DR   PFAM; PF00360; phytochrome; 1.
DR   PFAM; PF00512; signal; 1.
DR   PFAM; PF00989; PAS; 2.
DR   MENDEL; 10718; SOLtu;PhyB;1.
KW   TRANSCRIPTION REGULATION; PHOTORECEPTOR; PHYTOCHROME; CHROMOPHORE;
KW   MULTIGENE FAMILY.
FT   BINDING     333    333       CHROMOPHORE.
SQ   SEQUENCE   1129 AA;  125621 MW;  B28F4323 CRC32;

  Query Match           70.4%;  Score 1027;  DB 1;  Length 1129;
  Best Local Similarity  74.7%;  Pred. No. 6.06e-227;
  Matches   142;  Conservative   23;  Mismatches  16;  Indels   9;  Gaps   3;

Db    227 GTLKLLCDTVVESVRELTGYDRVMVYKFHEDEHGEVVAESKRSDLEPYIGLHYPATDIPQ 286
          |  :  ||||||| |: |||||||||| ||||:|||||:| :|||||||:||||||||||
Qy     16 GDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDLEPYLGLHYPATDIPQ 75

Db    287 ASRFLFKQNRVRMIVDCHATPVRVTQDESLMQPLCLVGSTLRAPHGCHAQYMANMGSIAS 346
          |:||||||||||| ||:||||:| | | |::|||| ||||||||||:||||||||:||
Qy     76 AARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPHGCHTQYMANMGSVAS 135

Db    347 LTLAVIINGNDEEAVGGGRNSMRLWGLVVGHHTSVRSIPFPLRYACEFLMQAFGLQLNME 406
          |:||::::|:|  :      | :||||||||| | |:|||||||||||||||||||| ||
Qy    136 LALAIVVKGKD--S------S-KLWGLVVGHHCSPRYVPFPLRYACEFLMQAFGLQLQME 186

Db    407 LQLASQLSEK 416
          |||||||:||
Qy    187 LQLASQLAEK 196


RESULT   12
ID   PHY1_PHYPA     STANDARD;      PRT;  1132 AA.
AC   P36505;
DT   01-JUN-1994 (REL. 29, CREATED)
DT   01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT   01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE   PHYTOCHROME 1.
GN   PHY1.
OS   PHYSCOMITRELLA PATENS (MOSS).
OC   EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; BRYOPSIDA;
OC   BRYIDAE; FUNARIALES; FUNARIACEAE; PHYSCOMITRELLA.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 94039823.
RA   KOLUKISAOGLU H.U., BRAUN B., MARTIN W.F., SCHNEIDER-POETSCH H.A.W.;
RT   "Mosses do express conventional, distantly B-type-related
RT   phytochromes. Phytochrome of Physcomitrella patens (Hedw.).";
RL   FEBS LETT. 334:95-100(1993).
CC   -!- FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT
CC       ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS
CC       MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PFR FORM THAT
CC       ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN
CC       PFR INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS
CC       RECONVERSION OF PFR TO PR CANCELS THE INDUCTION OF THOSE
CC       RESPONSES. PFR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR
CC       GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-
CC       BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN,
CC       PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS
CC       THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION.
CC   -!- SUBUNIT: HOMODIMER.
CC   -!- PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X75025; G402606; -.
DR   PIR; S37206; S37206.
DR   PROSITE; PS00245; PHYTOCHROME_1; 1.
DR   PROSITE; PS50046; PHYTOCHROME_2; 1.
DR   PFAM; PF00360; phytochrome; 1.
DR   PFAM; PF00512; signal; 1.
DR   PFAM; PF00989; PAS; 2.
KW   TRANSCRIPTION REGULATION; PHOTORECEPTOR; PHYTOCHROME; CHROMOPHORE.
FT   BINDING     321    321       CHROMOPHORE (BY SIMILARITY).
SQ   SEQUENCE   1132 AA;  125230 MW;  FC915B66 CRC32;

  Query Match           69.7%;  Score 1016;  DB 1;  Length 1132;
  Best Local Similarity  67.8%;  Pred. No. 4.44e-224;
  Matches   139;  Conservative   33;  Mismatches  24;  Indels   9;  Gaps   3;

Db    200 KLAAKAITRLQALPGGNIGLLCDTVVEEVRELTGYDRVMAYRFHEDEHGEVVAEIRRADL 259
          ||| :||:|||:||||:|| |||||||:|: ||||||| |:||||:||||||||:||
Qy      1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL 60

Db    260 EPYLGLHYPGTDIPQASRFLFMKNKVRIIADCSAPPVKVIQDPTLRQPVSLAGSTLRSPH 319
          |||||||||:||||||:|||| |:||:| ||:| ||||:|   |::|: |  ||||:||
Qy     61 EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120

Db    320 GCHAQYMGNMGSIASLVMAVIINDNEEDSHGSVQRGRKLWGLVVCHHTSPRTVPFPLRSA 379
          |||:|||:||||:||| :|:::: :  ||  |     ||||||| || ||| ||||||
Qy    121 GCHTQYMANMGSVASLALAIVVKGK--DS--S-----KLWGLVVGHHCSPRYVPFPLRYA 171

Db    380 CGFLMQVFGLQLNMEVESAAQLREK 404
          | |||| ||||| ||:: |:|| ||
Qy    172 CEFLMQAFGLQLQMELQLASQLAEK 196


RESULT   13
ID   PHY_PICAB      STANDARD;      PRT;  1136 AA.
AC   Q40762;
DT   01-NOV-1997 (REL. 35, CREATED)
DT   01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   PHYTOCHROME.
OS   PICEA ABIES (NORWAY SPRUCE) (PICEA EXCELSA).
OC   EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC   EUPHYLLOPHYTES; SPERMATOPHYTA; CONIFEROPSIDA; CONIFERALES; PINACEAE;
OC   PICEA.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   CLAPHAM D.H., LARSSON C.T., QAMARUDDIN M.;
RL   SUBMITTED (JUL-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
CC   -!- FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT
CC       ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS
CC       MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PFR FORM THAT
CC       ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN
CC       PFR INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS
CC       RECONVERSION OF PFR TO PR CANCELS THE INDUCTION OF THOSE
CC       RESPONSES. PFR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR
CC       GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-
CC       BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN,
CC       PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS
CC       THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION.
CC   -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
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CC   -!- PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.
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CC   ---------------------------------------------------------------------
DR   EMBL; U60264; G1399958; -.
DR   PROSITE; PS00245; PHYTOCHROME_1; 1.
DR   PROSITE; PS50046; PHYTOCHROME_2; 1.
DR   PFAM; PF00360; phytochrome; 1.
DR   PFAM; PF00512; signal; 1.
DR   PFAM; PF00989; PAS; 2.
KW   TRANSCRIPTION REGULATION; PHOTORECEPTOR; PHYTOCHROME; CHROMOPHORE.
FT   BINDING     336    336       CHROMOPHORE (BY SIMILARITY).
SQ   SEQUENCE   1136 AA;  126066 MW;  AD812130 CRC32;

  Query Match           68.3%;  Score 996;  DB 1;  Length 1136;
  Best Local Similarity  68.9%;  Pred. No. 7.13e-219;
  Matches   144;  Conservative   28;  Mismatches  24;  Indels  13;  Gaps   3;

Db    215 KLAAKAISRLQSLPGGDIRLLCDTVVQEVRELTGYDRVMAYRFHEDEHGEVVAEMRRPDL 274
          ||| :|||||||||||||  |||||||::|: |||||||| |:||||:|||||:|:||:||
Qy      1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL 60

Db    275 EPYLGLHYPATDIPQASRFLFMKNRVRMICDCCAPPVNVIQDKRLRQPLSLCGSTLRAPH 334
          ||||||||||||||||:||||: |||||||||  | ||:|:|   |::|| |  |||||||
Qy     61 EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120

Db    335 GCHAQYMANMGSIASLVMSVTTNENGDDSEGGGQQQPQNRRKLWGLVVCHHTSPRVIPFP 394
          |||:||||||||:||| :::  :  | ||         :  |||||||  || ||| :|||
Qy    121 GCHTQYMANMGSVASLALAIVVK--GKDS---------S--KLWGLVVGHHCSPRYVPFP 167

Db    395 LRYACEFLMQVFGIQLNKEVELAAQLREK 423
          |||||||||| |||:|| :|::||:|| ||
Qy    168 LRYACEFLMQAFGLQLQMELQLASQLAEK 196


RESULT   14
ID   PHY1_CERPU     STANDARD;      PRT;  1307 AA.
AC   P25848; P93100;
DT   01-MAY-1992 (REL. 22, CREATED)
DT   15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
DT   15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE   PHYTOCHROME / PROTEIN KINASE (EC 2.7.1.-).
GN   PHY1 OR PHY.
OS   CERATODON PURPUREUS (MOSS).
OC   EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; BRYOPSIDA;
OC   BRYIDAE; DICRANALES; DITRICHACEAE; CERATODON.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 93099252.
RA   THUEMMLER F., DUFNER M., KREISL P., DITTRICH P.;
RT   "Molecular cloning of a novel phytochrome gene of the moss Ceratodon
RT   purpureus which encodes a putative light-regulated protein kinase.";
RL   PLANT MOL. BIOL. 20:1003-1017(1992).
RN   [2]
RP   SEQUENCE OF 49-538 FROM N.A.
RX   MEDLINE; 91085543.
RA   THUEMMLER F., BEETZ A., RUEDIGER W.;
RT   "Phytochrome in lower plants. Detection and partial sequence of a
RT   phytochrome gene in the moss Ceratodon purpureus using the polymerase
RT   chain reaction.";
RL   FEBS LETT. 275:125-129(1990).
RN   [3]
RP   REVISIONS TO C-TERMINAL.
RC   STRAIN=WT3;
RA   PASENTSIS K., PAULO N., DITTRICH P., ALGARRA P., THUEMMLER F.,
RA   DUFNER M., KREISL P.;
RL   SUBMITTED (FEB-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
CC   -!- FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT
CC       ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS
CC       MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PFR FORM THAT
CC       ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN
CC       PFR INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS
CC       RECONVERSION OF PFR TO PR CANCELS THE INDUCTION OF THOSE
CC       RESPONSES. PFR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR
CC       GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-
CC       BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN,
CC       PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS
CC       THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION.
CC   -!- SUBUNIT: HOMODIMER.
CC   -!- SUBCELLULAR LOCATION: LOCATED IN A FIXED POSITION CLOSE TO THE
CC       PLASMA MEMBRANE.
CC   -!- PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.
CC   -!- SIMILARITY: IN THE C-TERMINAL, WITH THE CONSERVED CATALYTIC
CC       DOMAINS OF SER/THR-PROTEIN KINASES.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U87632; G1839248; -.
DR   EMBL; X17084; G296091; ALT_SEQ.
DR   PIR; S12966; S12966.
DR   PIR; S27396; S27396.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00245; PHYTOCHROME_1; 1.
DR   PROSITE; PS50046; PHYTOCHROME_2; 1.
DR   PFAM; PF00069; pkinase; 1.
DR   PFAM; PF00360; phytochrome; 1.
DR   PFAM; PF00989; PAS; 1.
DR   HSSP; P11362; 1FGI.
KW   TRANSCRIPTION REGULATION; PHOTORECEPTOR; PHYTOCHROME; CHROMOPHORE;
KW   TRANSFERASE; SERINE/THREONINE-PROTEIN KINASE; ATP-BINDING.
FT   DOMAIN        1    778       CHROMOPHORE BINDING DOMAIN.
FT   DOMAIN      779   1003       HINGE.
FT   DOMAIN     1004   1307       PROTEIN KINASE.
FT   BINDING     320    320       CHROMOPHORE (BY SIMILARITY).
FT   NP_BIND    1010   1018       ATP (BY SIMILARITY).
FT   BINDING    1031   1031       ATP (BY SIMILARITY).
FT   ACT_SITE   1127   1127       BY SIMILARITY.
SQ   SEQUENCE   1307 AA;  145843 MW;  910C665C CRC32;

  Query Match           67.6%;  Score 986;  DB 1;  Length 1307;
  Best Local Similarity  64.4%;  Pred. No. 2.85e-216;
  Matches   132;  Conservative   38;  Mismatches  26;  Indels   9;  Gaps   3;

Db    199 KLAARAITRLQALPGGDIELLCDTIVEEVRELTGYDRVMAFKFHEDEHGEVVAEIRRMDL 258
          ||| |||:|||:|||||  ||||:||:|: |||||||| : ||||:|||||:|||| ||
Qy      1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL 60

Db    259 EPYMGLHYPATDIPQASRFLLMKNRVRLIADCYASPVKLIQDPDIRQPVSLAGSTLRAPH 318
          |||:||||||||||||:|||:: ||||:| || |:|||::|  ::::|: |  |||||||
Qy     61 EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120

Db    319 GCHAQYMGNMGSIASLVMAVIINDNEEYSRGAIQRGRKLWGLVVCQHTSPRTVPFPLRSV 378
          |||:|||:||||:||| :|:::: ::  |  :     ||||||| :| ||| ||||||
Qy    121 GCHTQYMANMGSVASLALAIVVKGKD--S--S-----KLWGLVVGHHCSPRYVPFPLRYA 171

Db    379 CEFLMQVFGMQLNLHVELAAQLREK 403
          |||||| ||:|| : ::||:|| ||
Qy    172 CEFLMQAFGLQLQMELQLASQLAEK 196


RESULT   15
ID   PHY_MOUSC      STANDARD;      PRT;  1124 AA.
```

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AC   P33529; Q40364;
DT   01-FEB-1994 (REL. 28, CREATED)
DT   01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT   01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE   PHYTOCHROME.
OS   MOUGEOTIA SCALARIS (HASSEL).
OC   EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; CHAROPHYTA; ZYGNEMATALES;
OC   ZYGNEMATACEAE; MOUGEOTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   WINANDS A., WAGNER G.;
RL   SUBMITTED (JUL-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
RN   [2]
RP   SEQUENCE OF 248-435 FROM N.A.
RX   MEDLINE; 93117305.
RA   WINANDS A., WAGNER G., MARX S., SCHNEIDER-POETSCH H.A.;
RT   "Partial nucleotide sequence of phytochrome from the zygnematophycean
RT   green alga Mougeotia.";
RL   PHOTOCHEM. PHOTOBIOL. 56:765-770(1992).
CC   -!- FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT
CC       ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE PR FORM THAT ABSORBS
CC       MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PFR FORM THAT
CC       ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN
CC       PFR INDUCES AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS
CC       RECONVERSION OF PFR TO PR CANCELS THE INDUCTION OF THOSE
CC       RESPONSES. PFR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR
CC       GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-
CC       BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN,
CC       PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS
CC       THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHION.
CC   -!- SUBUNIT: HOMODIMER.
CC   -!- PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X95550; E221402; -.
DR   EMBL; S52048; G262811; -.
DR   PROSITE; PS00245; PHYTOCHROME_1; 1.
DR   PROSITE; PS50046; PHYTOCHROME_2; 1.
DR   PFAM; PF00360; phytochrome; 1.
DR   PFAM; PF00512; signal; 1.
DR   PFAM; PF00989; PAS; 2.
KW   TRANSCRIPTION REGULATION; PHOTORECEPTOR; PHYTOCHROME; CHROMOPHORE.
FT   BINDING     325    325       CHROMOPHORE (BY SIMILARITY).
FT   CONFLICT    342    342       S -> C (IN REF. 2).
FT   CONFLICT    381    381       R -> H (IN REF. 2).
FT   CONFLICT    399    399       V -> A (IN REF. 2).
SQ   SEQUENCE   1124 AA;  123923 MW;  CFDC29F3 CRC32;

  Query Match           67.0%;  Score 977;  DB 1;  Length 1124;
  Best Local Similarity  64.4%;  Pred. No. 6.23e-214;
  Matches   132;  Conservative   31;  Mismatches  33;  Indels   9;  Gaps   3;

Db    204 KLAAKAISRLQSLPGGDICGLCDVVVEEVRELTGYDRVMAYKFHDDEHGEVVAEIRRSDL 263
          ||| :|||||||||||||| :||| |||:|: |||||||| | ||:|:|||||:|||||||
Qy      1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL 60

Db    264 EPYLGLHYPATDIPQASRFLFIKNRIRMICDCTSPQVKVVQDSRIPQEMSLAGSTMRGVH 323
          ||||||||||||||||:||||  ||:|||||| :  |||||   : : : |  ||:|: |
Qy     61 EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120

Db    324 GCHTQYMMNMGSTASLVMSVTINDTNEIAGGPGMKGRKLWGLIVCHHSTPRHIPFPIRSA 383
          ||||||| |||| ||| ::: ::  :: ::       |||||:| || :|| :|||:| |
Qy    121 GCHTQYMANMGSVASLALAIVVKG-KD-SS-------KLWGLVVGHHCSPRYVPFPLRYA 171

Db    384 CEFLMQVFGLQLNMEVELAAQHREK 408
          |||||| ||||| ||::||:|  ||

Qy    172 CEFLMQAFGLQLQMELQLASQLAEK 196

Search completed: Mon Sep 13 14:23:48 1999
Job time : 17 secs.
```

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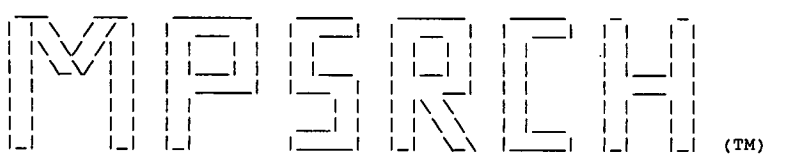

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Sep 13 14:24:04 1999; MasPar time 14.69 Seconds
728.410 Million cell updates/sec

Tabular output not generated.

Title: >US-09-272-809-9
Description: (1-196) from US09272809.pep
Perfect Score: 1458
Sequence: 1 KLAVRAISRLQSLPGGDIGA.....QAFGLQLQMELQLASQLAEK 196

Scoring table: PAM 150
Gap 11

Searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl9
1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 43.967; Variance 68.271; scale 0.644

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	1157	79.4	1135	10	O24117	PHYTOCHROME B.	4.28e-269
2	1133	77.7	1130	10	O24380	PHYTOCHROME B.	1.25e-262
3	1087	74.6	1039	10	P93527	PHYTOCHROME B (FRAGMEN	2.95e-250
4	1085	74.4	197	10	O04779	PHYTOCHROME E (FRAGMEN	1.02e-249
5	1056	72.4	196	10	O24404	PHYTOCHROME E (FRAGMEN	6.28e-242
6	1047	71.8	197	10	O04789	PHYTOCHROME E (FRAGMEN	1.64e-239
7	1045	71.7	193	10	O04762	PHYTOCHROME E (FRAGMEN	5.63e-239
8	1044	71.6	195	10	O04809	PHYTOCHROME E (FRAGMEN	1.04e-238
9	1039	71.3	1164	10	O23472	PHYTOCHROME D.	2.29e-237
10	1038	71.2	1140	10	O82148	PHYTOCHROME 2.	4.25e-237
11	1033	70.9	193	10	O24055	PHYTOCHROME E (FRAGMEN	9.33e-236
12	1031	70.7	191	10	O24069	PHYTOCHROME E (FRAGMEN	3.21e-235
13	1030	70.6	1118	10	O80419	PHYTOCHROME.	5.95e-235
14	1030	70.6	1121	10	O24446	PHYTOCHROME PHOTORECEP	5.95e-235
15	1026	70.4	198	10	P93524	PHYTOCHROME E (FRAGMEN	7.04e-234
16	1019	69.9	1142	10	Q40263	PHYTOCHROME.	5.30e-232
17	1011	69.3	192	10	O24278	PHYTOCHROME E (FRAGMEN	7.38e-230
18	1005	68.9	220	10	Q41333	PHYTOCHROME B2 (FRAGME	2.99e-228
19	1003	68.8	164	10	P93123	PHYTOCHROME E (FRAGMEN	1.03e-227
20	996	68.3	190	10	P93170	PHYTOCHROME E (FRAGMEN	7.70e-226
21	996	68.3	368	10	Q40917	PHYTOCHROME (FRAGMENT)	7.70e-226
22	990	67.9	221	10	Q41332	PHYTOCHROME B1 (FRAGME	3.11e-224
23	987	67.7	151	10	O04801	PHYTOCHROME E (FRAGMEN	1.98e-223
24	984	67.5	187	10	O04782	PHYTOCHROME E (FRAGMEN	1.26e-222
25	980	67.2	1299	10	P93098	PHOTORECEPTOR (FRAGMEN	1.48e-221
26	965	66.2	186	10	O24065	PHYTOCHROME E (FRAGMEN	1.52e-217
27	959	65.8	184	10	P93145	PHYTOCHROME E (FRAGMEN	6.12e-216
28	959	65.8	1135	10	P93528	PHYTOCHROME C.	6.12e-216
29	898	61.6	200	10	O04805	PHYTOCHROME B (FRAGMEN	1.17e-199
30	888	60.9	188	10	O09240	PODOCARPUS NERIIFOLIUS	5.42e-197
31	885	60.7	187	10	Q39771	PHYTOCHROME (FRAGMENT)	3.41e-196
32	850	58.3	1131	10	P93526	PHYTOCHROME A.	6.99e-187
33	839	57.5	189	10	O04416	PHYTOCHROME (FRAGMENT)	5.84e-184
34	815	55.9	193	10	O04413	PHYTOCHROME (FRAGMENT)	1.37e-177
35	804	55.1	156	10	Q40756	PHYTOCHROME (FRAGMENT)	1.13e-174
36	803	55.1	190	10	O04802	PHYTOCHROME B (FRAGMEN	2.07e-174
37	773	53.0	190	10	Q40304	PHYTOCHROME (FRAGMENT)	1.80e-166
38	770	52.8	190	10	Q96402	PHYTOCHROME (FRAGMENT)	1.12e-165
39	768	52.7	190	10	O04411	PHYTOCHROME (FRAGMENT)	3.78e-165
40	763	52.3	146	10	P93061	PHYTOCHROME E (FRAGMEN	7.93e-164
41	759	52.1	191	10	O04412	PHYTOCHROME (FRAGMENT)	9.03e-163
42	757	51.9	215	10	O22569	PHYTOCHROME A (FRAGMEN	3.05e-162
43	753	51.6	190	10	Q38699	PHYTOCHROME (FRAGMENT)	3.47e-161
44	753	51.6	190	10	Q40747	PHYTOCHROME (FRAGMENT)	3.47e-161
45	746	51.2	190	10	O09235	PHYTOCHROME (FRAGMENT)	2.44e-159

ALIGNMENTS

```
RESULT    1
ID   O24117      PRELIMINARY;      PRT;  1135 AA.
AC   O24117;
DT   01-JAN-1998 (TREMBLREL. 05, CREATED)
DT   01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT   01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE   PHYTOCHROME B.
GN   PHYB.
OS   NICOTIANA PLUMBAGINIFOLIA (LEADWORT-LEAVED TOBACCO).
OC   EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC   EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
OC   ASTERIDAE; SOLANANAE; SOLANALES; SOLANACEAE; NICOTIANA.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. PBH1D; TISSUE=LEAF;
RA   HUDSON M.E., ROBSON P.R.H., KRAEPIEL Y., CABOCHE M., SMITH H.;
RL   SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; Y14676; E339604; -.
DR   PROSITE; PS00245; PHYTOCHROME_1; 1.
DR   PFAM; PF00360; phytochrome; 1.
DR   PFAM; PF00512; signal; 1.
DR   PFAM; PF00989; PAS; 2.
KW   PHYTOCHROME.
SQ   SEQUENCE   1135 AA;  125810 MW;  BB76B292 CRC32;

  Query Match           79.4%;  Score 1157;  DB 10;  Length 1135;
  Best Local Similarity 77.5%;  Pred. No. 4.28e-269;
  Matches   158;  Conservative   25;  Mismatches  13;  Indels   8;  Gaps   2;

Db    217 KLAVRAISHLQSLPGGDVKILCDTVVESVRELTGYDRVMVYKFHEDEHGEVVAESKRPDL 276
          ||||||||:||||||||:  ||||||| |: |||||||||| ||||:|||||:| :|:||
Qy      1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL 60

Db    277 EPYIGLHYPATDIPQASRFLFKQNRVRMIVDCHATPVRVVQDESLMQPLCLVGSTLRAPH 336
          |||:||||||||||||:|||||||||||| ||:||||:||| | |::|||||| |||||||
Qy     61 EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120

Db    337 GCHAQYMANMGSIASLTLAVIINGNDEEAVGGRSSMRLWGLVVGHHTSARCIPFPLRYAC 396
          |||:|||||||:|||:||:::::|:|       || :|||||||| |:| :||||||||
Qy    121 GCHTQYMANMGSVASLALAIVVKGKD-------SS-KLWGLVVGHHCSPRYVPFPLRYAC 172

Db    397 EFLMQAFGLQLNMELQLASQLSEK 420
          |||||||||| |||||||||:||
Qy    173 EFLMQAFGLQLQMELQLASQLAEK 196
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RESULT    2
ID   O24380      PRELIMINARY;      PRT;  1130 AA.
AC   O24380;
DT   01-JAN-1998 (TREMBLREL. 05, CREATED)
DT   01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT   01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE   PHYTOCHROME B.
GN   PHYB.
OS   SOLANUM TUBEROSUM (POTATO).
OC   EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC   EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS;
OC   ASTERIDAE; SOLANANAE; SOLANALES; SOLANACEAE; SOLANUM.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. DESIREE; TISSUE=LEAF;
RA   GATZ C.;
RL   SUBMITTED (AUG-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. DESIREE; TISSUE=LEAF;
RX   MEDLINE; 93081720.
RA   HEYER A., GATZ C.;
RT   "Isolation and characterization of a cDNA-clone coding for potato
RT   type B phytochrome.";
RL   PLANT MOL. BIOL. 20:589-600(1992).
DR   EMBL; Y14572; E333043; -.
DR   PROSITE; PS00245; PHYTOCHROME_1; 1.
DR   PFAM; PF00360; phytochrome; 1.
DR   PFAM; PF00512; signal; 1.
DR   PFAM; PF00989; PAS; 2.
KW   PHYTOCHROME.
SQ   SEQUENCE   1130 AA;  125421 MW;  34A87DFA CRC32;

  Query Match           77.7%;  Score 1133;  DB 10;  Length 1130;
  Best Local Similarity  77.1%;  Pred. No. 1.25e-262;
  Matches   158;  Conservative   23;  Mismatches  15;  Indels   9;  Gaps   3;

Db    211 KLAVRAISHLQSLPGGDIKLLCDTVVESVRELTGYDRVMVYKFHEDEHGEVVAESKRSDL 270
          |||||||:|||||||||  |||||| |: |||||||||| ||||:|||||:| :||||
Qy      1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL 60

Db    271 EPYIGLHYPATDIPQASRFLFKQNRVRMIVDCHATPVRVTQDESLMQPLCLVGSTLRAPH 330
          |||:|||||||||||||:|||||||||||| ||:||||:| | | |::||||| |||||||
Qy     61 EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120

Db    331 GCHAQYMANMGSIASLTLAVIINGNDEEAVGGGRNSMRLWGLVVGHHTSVRSIPFPLRYA 390
          |||:|||||||||:|||:||::::|:|  :      | :|||||||| | | :|||||||
Qy    121 GCHTQYMANMGSVASLALAIVVKGKD--S------S-KLWGLVVGHHCSPRYVPFPLRYA 171

Db    391 CEFLMQAFGLQLNMELQLASQLSEK 415
          |||||||||||| |||||||||:||
Qy    172 CEFLMQAFGLQLQMELQLASQLAEK 196


RESULT    3
ID   P93527      PRELIMINARY;      PRT;  1039 AA.
AC   P93527;
DT   01-MAY-1997 (TREMBLREL. 03, CREATED)
DT   01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT   01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
DE   PHYTOCHROME B (FRAGMENT).
GN   PHYB.
OS   SORGHUM BICOLOR MILO (SORGHUM).
OC   EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC   EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES;
OC   POACEAE; SORGHUM.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. 58M;
RA   CHILDS K.L., MILLER F.R., CORDONNIER-PRATT M.M., PRATT L.H.,
RA   MORGAN P.W., MULLET J.E.;
RL   SUBMITTED (APR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; U56730; G1800217; -.
DR   PROSITE; PS00245; PHYTOCHROME_1; 1.
DR   PFAM; PF00360; phytochrome; 1.
DR   PFAM; PF00512; signal; 1.
DR   PFAM; PF00989; PAS; 2.
DR   MENDEL; 10742; SORbi;PhyB;1.
KW   PHYTOCHROME.
FT   NON_TER       1      1
SQ   SEQUENCE   1039 AA;  115167 MW;  CA4C1B9A CRC32;

  Query Match           74.6%;  Score 1087;  DB 10;  Length 1039;
  Best Local Similarity  74.5%;  Pred. No. 2.95e-250;
  Matches   155;  Conservative   21;  Mismatches  20;  Indels  12;  Gaps   3;

Db    112 KLAVRAISRLQALPGGDIKLLCDTVVEHVRELTGYDRVMVYRFHEDEHGEVVAESRRDNL 171
          ||||||||||:|||||  ||||||| |: |||||||||:||||:|||||:| || :|
Qy      1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL 60

Db    172 EPYLGLHYPATDIPQASRFLFRQNRVRMIADCHATPVRVIQDPGMSQPLCLVGSTLRAPH 231
          ||||||||||||||||:||||:||||||| ||:||||:|:|   : :||||| |||||||
Qy     61 EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120

Db    232 GCHAQYMANMGSIASLVMAVIISSGGDDEQTGRGGISSAMKLWGLVVCHHTSPRCIPFPL 291
          |||:||||||||:||| :|:::   | |        ||  ||||||| || ||| :||||
Qy    121 GCHTQYMANMGSVASLALAIVVK--GKD--------SS--KLWGLVVGHHCSPRYVPFPL 168

Db    292 RYACEFLMQAFGLQLNMELQLAHQLSEK 319
          |||||||||||||||| |||||| ||:||
Qy    169 RYACEFLMQAFGLQLQMELQLASQLAEK 196


RESULT    4
ID   O04779      PRELIMINARY;      PRT;   197 AA.
AC   O04779;
DT   01-JUL-1997 (TREMBLREL. 04, CREATED)
DT   01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT   01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
DE   PHYTOCHROME E (FRAGMENT).
GN   PHYE.
OS   CARMICHAELIA SP. 'LAVIN 6201'.
OC   EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC   EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
OC   FABALES; FABACEAE; PAPILIONOIDEAE; CARMICHAELIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   LAVIN M., ESHBAUGH E., HU J.-M., MATHEWS S., SHARROCK R.A.;
RL   AM. J. BOT. 85:412-433(1998).
DR   EMBL; U78839; G1711068; -.
DR   PROSITE; PS00245; PHYTOCHROME_1; 1.
DR   PFAM; PF00360; phytochrome; 1.
DR   MENDEL; 14081; CARss;2331;mn14081.
KW   PHYTOCHROME.
FT   NON_TER       1      1
FT   NON_TER     197    197
SQ   SEQUENCE   197 AA;  22597 MW;  05DAFB24 CRC32;

  Query Match           74.4%;  Score 1085;  DB 10;  Length 197;
  Best Local Similarity  84.0%;  Pred. No. 1.02e-249;
  Matches   136;  Conservative   18;  Mismatches   8;  Indels   0;  Gaps   0;

Db      1 YDRVMAYKFHEDDHGEVVSEIRRSDLEPYLGLHYPSTDIPQAARFLFKQNRVRMICDCHA 60
          ||||| | |||||||||||||||||||||||:|||||||||||||||||||||:|
Qy     35 YDRVMVYQFHEDDHGEVVSEIRRSDLEPYLGLHYPATDIPQAARFLFKQNRVRMICDCNA 94

Db     61 KPVKVIQSEELRQPLCLVNSTLRSPHDCHTQYMANMGSIASLVMAVIVNGNDSTRLWGLL 120
            ||||:|||||::|||||||||:|| |||||||||||:||| :|::|:|:|:||::|||||:
Qy     95 TPVKVVQSEELKRPLCLVNSTLRAPHGCHTQYMANMGSVASLALAIVVKGKDSSKLWGLV 154

Db    121 VCHHSSPRYVPFPVRYACEFLMQAFGLQLYMEIQLASQMAEK 162
          | || ||||||||:|||||||||||||| ||:|||||:|||
Qy    155 VGHHCSPRYVPFPLRYACEFLMQAFGLQLQMELQLASQLAEK 196
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```
RESULT    5
ID   O24404      PRELIMINARY;      PRT;   196 AA.
AC   O24404;
DT   01-JAN-1998 (TREMBLREL. 05, CREATED)
DT   01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
DT   01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE   PHYTOCHROME E (FRAGMENT).
GN   PHYE.
OS   TEPHROSIA VILLOSA.
OC   EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC   EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
OC   FABALES; FABACEAE; PAPILIONOIDEAE; TEPHROSIA.
RN   [1]
PP   SEQUENCE FROM N.A.
RA   LAVIN M., ESHBAUGH E., HU J.-M., MATHEWS S., SHARROCK R.A.;
RL   AM. J. BOT. 85:412-433(1998).
DR   EMBL; AF004796; G3176541; -.
DR   PROSITE; PS00245; PHYTOCHROME_1; 1.
DR   PFAM; PF00360; phytochrome; 1.
KW   PHYTOCHROME.
FT   NON_TER       1      1
FT   NON_TER     196    196
SQ   SEQUENCE   196 AA;  22424 MW;  0FB3DD8C CRC32;

  Query Match           72.4%;  Score 1056;  DB 10;  Length 196;
  Best Local Similarity  82.0%;  Pred. No. 6.28e-242;
  Matches   132;  Conservative   21;  Mismatches   8;  Indels   0;  Gaps   0;

Db      1 DRVMAYKFHEDDHGEVIAEIRRSDLEPYLGLHYPATDIPQASRFLFKQNRVRMICDCHAK 60
          |||| | |||||||||::||||||||||||||||||||||||:|||||||||||||||:|
Qy     36 DRVMVYQFHEDDHGEVVSEIRRSDLEPYLGLHYPATDIPQAARFLFKQNRVRMICDCNAT 95

Db     61 PVKVIQSEELRQSLCLVNSTLRSPHVCHTQYMANMGSIASLVMAIIVNGNDTTRLWGLLV 120
          ||||:|||||:::|||||||||:|| |||||||||||:||| :||:|:|:|:::||||:|
Qy     96 PVKVVQSEELKRPLCLVNSTLRAPHGCHTQYMANMGSVASLALAIVVKGKDSSKLWGLVV 155

Db    121 CHHTSPRYVPFPVRYACEFLMQAFGLQLYMEIQLASQMAEK 161
           || |||||||:|||||||||||||| ||:|||||:|||
Qy    156 GHHCSPRYVPFPLRYACEFLMQAFGLQLQMELQLASQLAEK 196


RESULT    6
ID   O04789      PRELIMINARY;      PRT;   197 AA.
AC   O04789;
DT   01-JUL-1997 (TREMBLREL. 04, CREATED)
DT   01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT   01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
DE   PHYTOCHROME E (FRAGMENT).
GN   PHYE.
OS   ENTEROLOBIUM CYCLOCARPUM.
OC   EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC   EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
OC   FABALES; FABACEAE; MIMOSOIDEAE; ENTEROLOBIUM.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   LAVIN M., ESHBAUGH E., HU J.-M., MATHEWS S., SHARROCK R.A.;
RL   AM. J. BOT. 85:412-433(1998).
DR   EMBL; U78827; G1711080; -.
DR   PROSITE; PS00245; PHYTOCHROME_1; 1.
DR   PFAM; PF00360; phytochrome; 1.
DR   MENDEL; 14091; ENTcy;2331;mn14091.
KW   PHYTOCHROME.
FT   NON_TER       1      1
FT   NON_TER     197    197
SQ   SEQUENCE   197 AA;  22645 MW;  E468A5CD CRC32;

  Query Match           71.8%;  Score 1047;  DB 10;  Length 197;
  Best Local Similarity  81.5%;  Pred. No. 1.64e-239;
  Matches   132;  Conservative   19;  Mismatches  11;  Indels   0;  Gaps   0;

Db      1 YDRVMAYKFHEDDHGEVVSEIRRSDLEPFFGLHYPATDIPQAARFLFKQNRVRMICDCHA 60
          ||||| | |||||||||||||||||||::|||||||||||||||||||||||||||||:|
Qy     35 YDRVMVYQFHEDDHGEVVSEIRRSDLEPYLGLHYPATDIPQAARFLFKQNRVRMICDCNA 94

Db     61 NPVKVIQSEESRQPLCLVNSTLRSPHQCHAQYMENMGSIASLVMAVIVNGNDTTKLWGLL 120
          ||||:|||| ::|||||||||||:|| ||:||| |||||||| :|::|:|:|::|||||:
Qy     95 TPVKVVQSEELKRPLCLVNSTLRAPHGCHTQYMANMGSVASLALAIVVKGKDSSKLWGLV 154

Db    121 VCHHTSPRHVPFPLRYACEFLMQAFGLQLYMEMQLASQMAEK 162
          | || ||| |||||||||||||||||||| ||:|||||:|||
Qy    155 VGHHCSPRYVPFPLRYACEFLMQAFGLQLQMELQLASQLAEK 196


RESULT    7
ID   O04762      PRELIMINARY;      PRT;   193 AA.
AC   O04762;
DT   01-JUL-1997 (TREMBLREL. 04, CREATED)
DT   01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
DT   01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
DE   PHYTOCHROME E (FRAGMENT).
GN   PHYE.
OS   AUSTROSTEENISIA BLACKII.
OC   EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC   EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
OC   FABALES; FABACEAE; PAPILIONOIDEAE; AUSTROSTEENISIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   LAVIN M., ESHBAUGH E., HU J.-M., MATHEWS S., SHARROCK R.A.;
RL   AM. J. BOT. 85:412-433(1998).
DR   EMBL; U78843; G3176474; -.
DR   PROSITE; PS00245; PHYTOCHROME_1; 1.
DR   PFAM; PF00360; phytochrome; 1.
DR   MENDEL; 14070; AUSbl;2331;mn14070.
KW   PHYTOCHROME.
FT   NON_TER       1      1
FT   NON_TER     193    193
SQ   SEQUENCE   193 AA;  22073 MW;  328BA8FA CRC32;

  Query Match           71.7%;  Score 1045;  DB 10;  Length 193;
  Best Local Similarity  83.5%;  Pred. No. 5.63e-239;
  Matches   132;  Conservative   17;  Mismatches   9;  Indels   0;  Gaps   0;

Db      1 MAYKFHEDDHGEVVSEIRRSDLEPYLGLHYPATDIPQASRFLFKQNRVRMICDCHAKPVK 60
          | | |||||||||||||||||||||||||||||||:|||||||||||||||:| |||
Qy     39 MVYQFHEDDHGEVVSEIRRSDLEPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVK 98

Db     61 VIQSEELRQPLCLVNSTLRSPHGCHTQYMANMGSIASLVMAVTVNGNDTRRLWGLLVCHH 120
          |:|||||::|||||||||:|||||||||||||||:||| :|: |:|:|: :||||:| ||
Qy     99 VVQSEELKRPLCLVNSTLRAPHGCHTQYMANMGSVASLALAIVVKGKDSSKLWGLVVGHH 158

Db    121 TSPRYVPFPVRYACEFLMQAFGLQLYMEIQLASQMAEK 158
           ||||||||:|||||||||||||| ||:|||||:|||
Qy    159 CSPRYVPFPLRYACEFLMQAFGLQLQMELQLASQLAEK 196


RESULT    8
ID   O04809      PRELIMINARY;      PRT;   195 AA.
AC   O04809;
DT   01-JUL-1997 (TREMBLREL. 04, CREATED)
DT   01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
DT   01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
DE   PHYTOCHROME E (FRAGMENT).
GN   PHYE.
OS   POECILANTHE FALCATA.
OC   EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC   EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
OC   FABALES; FABACEAE; PAPILIONOIDEAE; POECILANTHE.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   LAVIN M., ESHBAUGH E., HU J.-M., MATHEWS S., SHARROCK R.A.;
RL   AM. J. BOT. 85:412-433(1998).
DR   EMBL; U78848; G3176484; -.
DR   PROSITE; PS00245; PHYTOCHROME_1; 1.
DR   PFAM; PF00360; phytochrome; 1.
DR   MENDEL; 14101; POEfa;2331;mn14101.
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KW   PHYTOCHROME.
FT   NON_TER       1      1
FT   NON_TER     195    195
SQ   SEQUENCE   195 AA;  22335 MW;  8A231B4E CRC32;

  Query Match           71.6%;  Score 1044;  DB 10;  Length 195;
  Best Local Similarity  83.1%;  Pred. No. 1.04e-238;
  Matches   133;  Conservative   18;  Mismatches   9;  Indels   0;  Gaps   0;

Db      1 RVMAYKFHEDDHGEVVSEIRRSDLEPYLGLHYPAKDIPQAARFLFKQNRVRMIFDCHAKP 60
          ||| | |||||||||||||||||||||||||||| |||||||||||||||||| ||:| |
Qy     37 RVMVYQFHEDDHGEVVSEIRRSDLEPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATP 96

Db     61 VNVIQSEELRQPLCLVNSTLRSPHGCHTQYMANMGSVASLVMAVIVNGNDTTRLWGLLVC 120
          |:|:||||||::|||||||||:|||||||||||||||| :|::|:|:|:::||||:|
Qy     97 VKVVQSEELKRPLCLVNSTLRAPHGCHTQYMANMGSVASLALAIVVKGKDSSKLWGLVVG 156

Db    121 HHTSPRYVPFPVRYACEFLMQAFGLQLYMEIQLATQLAEK 160
          || ||||||||:|||||||||||||| ||:|||:|||||
Qy    157 HHCSPRYVPFPLRYACEFLMQAFGLQLQMELQLASQLAEK 196


RESULT    9
ID   O23472      PRELIMINARY;      PRT;  1164 AA.
AC   O23472;
DT   01-JAN-1998 (TREMBLREL. 05, CREATED)
DT   01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT   01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE   PHYTOCHROME D.
OS   ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
OC   EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC   EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
OC   CAPPARALES; BRASSICACEAE; ARABIDOPSIS.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   EU ARABIDOPSIS SEQUENCING PROJECT, ESSA;
RL   SUBMITTED (JUN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 98121113.
RA   BEVAN M., BANCROFT I., BENT E., LOVE K., GOODMAN H., DEAN C.,
RA   BERGKAMP R., DIRKSE W., VAN STAVEREN M., STIEKEMA W., DROST L.,
RA   RIDLEY P., HUDSON S.A., PATEL K., MURPHY G., PIFFANELLI P., WEDLER H.,
RA   WEDLER E., WAMBUTT R., WEITZENEGGER T., POHL T.M., TERRYN N.,
RA   GIELEN J., VILLARROEL R., DE CLERCK R., VAN MONTAGU M., LECHARNY A.,
RA   AUBORG S., GY I., KREIS M., LAO N., KAVANAGH T., HEMPEL S., KOTTER P.,
RA   ENTIAN K.D., RIEGER M., SCHAEFFER M., FUNK B., MUELLER-AUER S.,
RA   SILVEY M., JAMES R., MONTFORT A., PONS A., PUIGDOMENECH P., DOUKA A.,
RA   VOUKELATOU E., MILIONI D., HATZOPOULOS P., PIRAVANDI E., OBERMAIER B.,
RA   HILBERT H., DUESTERHOFT A., MOORES T., JONES J.D.G., ENEVA T.,
RA   PALME K., BENES V., RECHMAN S., ANSORGE W., COOKE R., BERGER C.,
RA   DELSENY M., VOET M., VOLCKAERT G., MEWES H.W., KLOSTERMAN S.,
RA   SCHUELLER C., CHALWATZIS N.;
RT   "Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of
RT   Arabidopsis thaliana.";
RL   NATURE 391:485-488(1998).
DR   EMBL; Z97340; E326982; -.
DR   PROSITE; PS00245; PHYTOCHROME_1; 1.
DR   PFAM; PF00360; phytochrome; 1.
DR   PFAM; PF00512; signal; 1.
DR   PFAM; PF00989; PAS; 2.
KW   PHYTOCHROME.
SQ   SEQUENCE   1164 AA;  129267 MW;  994EB82E CRC32;

  Query Match           71.3%;  Score 1039;  DB 10;  Length 1164;
  Best Local Similarity  71.6%;  Pred. No. 2.29e-237;
  Matches   149;  Conservative   29;  Mismatches  18;  Indels  12;  Gaps   4;

Db    239 KLAVRAISHLQSLPSGDIKLLCDTVVESVRDLTGYDRVMVYKFHEDEHGEVVAESKRNDL 298
          ||||||||:|||||:|||  ||||||| |: ||||||||||| ||||:|||||:| :|:||
Qy      1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL 60

Db    299 EPYIGLHYPATDIPQASRFLFKQNRVRMIVDCYASPVRVVQDDRLTQFICLVGSTLRAPH 358
          |||:||||||||||:|||||||||||| || |:||:||| : | : :||| |||||||
Qy     61 EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120

Db    359 GCHAQYMTNMGSIASLAMAVIINGNEEDGNGVNTGGRNSMRLWGLVVCHHTSARCIPFPL 418
          |||:|||:||||:||||:|:::::|:  |      :    | :|||||| || |:| :||||
Qy    121 GCHTQYMANMGSVASLALAIVVKGK--D-----S----S-KLWGLVVGHHCSPRYVPFPL 168

Db    419 RYACEFLMQAFGLQLNMELQLALQVSEK 446
          |||||||||||||| |||||| |::||
Qy    169 RYACEFLMQAFGLQLQMELQLASQLAEK 196


RESULT   10
ID   O82148      PRELIMINARY;      PRT;  1140 AA.
AC   O82148;
DT   01-NOV-1998 (TREMBLREL. 08, CREATED)
DT   01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT   01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE   PHYTOCHROME 2.
GN   PHY2.
OS   ADIANTUM CAPILLUS-VENERIS (FERN).
OC   EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC   EUPHYLLOPHYTES; FILICOPHYTA; FILICOPSIDA; FILICALES; ADIANTACEAE;
OC   ADIANTUM.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LEAF;
RA   NOZUE K., FUKUDA S., KANEGAE T., WADA M.;
RT   "Isolation of a second phytochrome cDNA from Adiantum
RT   capillus-veneris (Accession no. AB016232).";
RL   PLANT PHYSIOL. 0:0-0(1998).
DR   EMBL; AB016232; D1034746; -.
DR   PROSITE; PS00245; PHYTOCHROME_1; 1.
KW   PHYTOCHROME.
SQ   SEQUENCE   1140 AA;  126523 MW;  7E83EB2C CRC32;

  Query Match           71.2%;  Score 1038;  DB 10;  Length 1140;
  Best Local Similarity  71.0%;  Pred. No. 4.25e-237;
  Matches   147;  Conservative   25;  Mismatches  24;  Indels  11;  Gaps   4;

Db    220 KLAAKAISRLQALPVGDIDLLCDSVVEEVRELTGYDRVMAYKFHEDEHGEVLAEIRRSDL 279
          ||| :||||||:|| |||  |||:|||:|: |||||||| | ||||:||||::|||||||
Qy      1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL 60

Db    280 EPYLGLHYPATDIPQASRFLFMKNRVRMICDCRALPVRVIQDKELRQPLSLAGSTLRAPH 339
          |||||||||||||||:||||: |||||||| | ||:|:|  ||::|| |  |||||||
Qy     61 EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120

Db    340 GCHSQYMANMGSIASLVMAVVVNDNDEDVSNRSQQPKMRRLWGLVVCHHTTPRAVPFALR 399
          |||:||||||||:||| :|:||: :|   |  |   |   |||||| || :|| |||:||
Qy    121 GCHTQYMANMGSVASLALAIVVKGKD---S--S---K---LWGLVVGHHCSPRYVPFPLR 169

Db    400 SACEFLMQVFGLQLNMELELAAQMREK 426
          .|||||| ||||| |||:||:|: ||
Qy    170 YACEFLMQAFGLQLQMELQLASQLAEK 196


RESULT   11
ID   O24055      PRELIMINARY;      PRT;   193 AA.
AC   O24055;
DT   01-JAN-1998 (TREMBLREL. 05, CREATED)
DT   01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
DT   01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE   PHYTOCHROME E (FRAGMENT).
GN   PHYE.
OS   MILLETTIA DURA.
OC   EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC   EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
OC   FABALES; FABACEAE; PAPILIONOIDEAE; MILLETTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   LAVIN M., ESHBAUGH E., HU J.-M., MATHEWS S., SHARROCK R.A.;
RL   AM. J. BOT. 85:412-433(1998).
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DR   EMBL; AF004785; G3176519; -.
DR   PROSITE; PS00245; PHYTOCHROME_1; 1.
DR   PFAM; PF00360; phytochrome; 1.
KW   PHYTOCHROME.
FT   NON_TER       1      1
FT   NON_TER     193    193
SQ   SEQUENCE   193 AA;  21970 MW;  D159ACD9 CRC32;

  Query Match           70.9%;  Score 1033;  DB 10;  Length 193;
  Best Local Similarity  84.2%;  Pred. No. 9.33e-236;
  Matches   133;  Conservative   14;  Mismatches  11;  Indels   0;  Gaps   0;

Db      1 MAYKFHEDDHGEVVSEIRRSDLEPYLGLHYPATDIPQASRFLFKQNRVRMICDCGAKPVK 60
          | | |||||||||||||||||||||||||||||||||||:|||||||||||||||| | |||
Qy     39 MVYQFHEDDHGEVVSEIRRSDLEPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVK 98

Db     61 VIQSEELRQPLCLVNSTLRSPHVCHTQYMANMGSTASLVLAIIVNGNDTTRLWGLLVCHH 120
          |:||||::|||||||||:|| |||||||||| ||| |||:|:|:|:::||||:| ||
Qy     99 VVQSEELKRPLCLVNSTLRAPHGCHTQYMANMGSVASLALAIVVKGKDSSKLWGLVVGHH 158

Db    121 TSPRYVPFPVRYACEFLMQAFGLQLYMEIQLASQKAEK 158
              ||||||||:|||||||||||||||| ||:||||| |||
Qy    159 CSPRYVPFPLRYACEFLMQAFGLQLQMELQLASQLAEK 196


RESULT   12
ID   O24069      PRELIMINARY;      PRT;   191 AA.
AC   O24069;
DT   01-JAN-1998 (TREMBLREL. 05, CREATED)
DT   01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
DT   01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE   PHYTOCHROME E (FRAGMENT).
GN   PHYE.
OS   MILLETTIA RICHARDIANA.
OC   EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC   EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
OC   FABALES; FABACEAE; PAPILIONOIDEAE; MILLETTIA.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   LAVIN M., ESHBAUGH E., HU J.-M., MATHEWS S., SHARROCK R.A.;
RL   AM. J. BOT. 85:412-433(1998).
DR   EMBL; AF004786; G3176521; -.
DR   PROSITE; PS00245; PHYTOCHROME_1; 1.
DR   PFAM; PF00360; phytochrome; 1.
KW   PHYTOCHROME.
FT   NON_TER       1      1
FT   NON_TER     191    191
SQ   SEQUENCE   191 AA;  21908 MW;  7E5C91B0 CRC32;

  Query Match           70.7%;  Score 1031;  DB 10;  Length 191;
  Best Local Similarity  84.0%;  Pred. No. 3.21e-235;
  Matches   131;  Conservative   17;  Mismatches   8;  Indels   0;  Gaps   0;

Db      1 YKFHEDDHGEVVSEIRRSDLEPYLGLHYPATDIPQASRFLFKQNRVRMICDCHAKPVKVI 60
          | |||||||||||||||||||||||||||||||||||:|||||||||||||||:| ||||:
Qy     41 YQFHEDDHGEVVSEIRRSDLEPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVV 100

Db     61 QSEELRQPLCLVNSTLRSPHVCHTQYMANMGSIASLVMAIIVNGNDKTRLWGLLVCHHTS 120
          |||||::|||||||||||:|| |||||||||||:||| :|||:|:|:| ::||||:| || |
Qy    101 QSEELKRPLCLVNSTLRAPHGCHTQYMANMGSVASLALAIVVKGKDSSKLWGLVVGHHCS 160

Db    121 PRYVPFPVRYACEFLMQAFGLQLYMEIQLASQMAEK 156
              |||||||:|||||||||||||||| ||:|||||:|||
Qy    161 PRYVPFPLRYACEFLMQAFGLQLQMELQLASQLAEK 196


RESULT   13
ID   O80419      PRELIMINARY;      PRT;  1118 AA.
AC   O80419;
DT   01-NOV-1998 (TREMBLREL. 08, CREATED)
DT   01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
DT   01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE   PHYTOCHROME.
GN   PHY1.
OS   ADIANTUM CAPILLUS-VENERIS (FERN).
OC   EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC   EUPHYLLOPHYTES; FILICOPHYTA; FILICOPSIDA; FILICALES; ADIANTACEAE;
OC   ADIANTUM.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LEAF;
RA   NOZUE K., FUKUDA S., KANEGAE T., WADA M.;
RL   SUBMITTED (JUL-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=LEAF;
RA   WADA M., KANEGAE T., NOZUE K., FUKUDA S.;
RT   "Cryptogam phytochromes.";
RL   PLANT CELL ENVIRON. 20:685-690(1997).
DR   EMBL; AB016151; D1032671; -.
DR   PROSITE; PS00245; PHYTOCHROME_1; 1.
KW   PHYTOCHROME.
SQ   SEQUENCE   1118 AA;  123824 MW;  3805B45B CRC32;

  Query Match           70.6%;  Score 1030;  DB 10;  Length 1118;
  Best Local Similarity  68.8%;  Pred. No. 5.95e-235;
  Matches   141;  Conservative   28;  Mismatches  27;  Indels   9;  Gaps   3;

Db    196 KLAAKAIARLQSLPGGDIGLLCDSVVEEVHELTGFDRVMAYKFHEDEHGEVVAEIRRTDL 255
          ||| :||:|||||||||||| |||:|||:|: |||:|||| | ||||:|||||:||||:||
Qy      1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL 60

Db    256 EPYIGLHYPATDIPQAARFLFMKNRVRMICDCRLPPVKLIQDKTLSQPMSLTGSKLRAPH 315
          |||:|||||||||||||||: |||||||||    |||::|    | :|: |  | |||||
Qy     61 EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120

Db    316 GCHTQYMANMNSISSLVMAVIVNDSDDDSPGHSSQGIKLWGLVVCHHTSPRYVPFPVRSA 375
          |||||||||| |::|| :|::|: : |     ||   ||||||| || |||||||:| |
Qy    121 GCHTQYMANMGSVASLALAIVVK-GKD-----SS---KLWGLVVGHHCSPRYVPFPLRYA 171

Db    376 CEFLMQVFSLQLNMEVGMAAQVREK 400
          |||||| |:||| ||: :|:|: ||
Qy    172 CEFLMQAFGLQLQMELQLASQLAEK 196


RESULT   14
ID   O24446      PRELIMINARY;      PRT;  1121 AA.
AC   O24446;
DT   01-JAN-1998 (TREMBLREL. 05, CREATED)
DT   01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT   01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
DE   PHYTOCHROME PHOTORECEPTOR.
GN   CPPHY2.
OS   CERATODON PURPUREUS (MOSS).
OC   EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; BRYOPSIDA;
OC   BRYIDAE; DICRANALES; DITRICHACEAE; CERATODON.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=WT3;
RA   HUGHES J.E., LAMPARTER T., MITTMANN F.;
RL   PLANT PHYSIOL. 112:446-446(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=WT3;
RA   PASENTSIS K., PAULO N., DITTRICH P., ALGARRA P., THUEMMLER F.;
RL   SUBMITTED (OCT-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
DR   EMBL; U72993; G1674478; -.
DR   PROSITE; PS00245; PHYTOCHROME_1; 1.
DR   PFAM; PF00360; phytochrome; 1.
DR   PFAM; PF00512; signal; 1.
DR   PFAM; PF00989; PAS; 2.
KW   PHYTOCHROME.
SQ   SEQUENCE   1121 AA;  124211 MW;  6EEDFE9F CRC32;

  Query Match           70.6%;  Score 1030;  DB 10;  Length 1121;
  Best Local Similarity  69.3%;  Pred. No. 5.95e-235;
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  Matches   142;  Conservative   31;  Mismatches  23;  Indels   9;  Gaps   3;

Db    198 KLAAKAITRLQALPGGDIGLLCDTVVEEVRELTGYDRVMAYKFHEDEHGEVVAEIRRMDL 257
          ||| :||:|||:|||||||  |||||||:|: ||||||||  | ||||:|||||:|||| ||
Qy      1 KLAVRAISRLQSLPGGDIGALCDTVVEDVQRLTGYDRVMVYQFHEDDHGEVVSEIRRSDL 60

Db    258 EPYLGLHYPATDIPQASRFLFMKNRVRVIADCCASPVKLIQDPDIKQPVSLAGSTLRAPH 317
          ||||||||||||||||:||||: ||||:| || |:|||::|  ::|:|: |  |||||||
Qy     61 EPYLGLHYPATDIPQAARFLFKQNRVRMICDCNATPVKVVQSEELKRPLCLVNSTLRAPH 120

Db    318 GCHAQYMGNMGSIASLVMAVIINDNEEDSRGAIQRGRKLWGLVVCHHTSPRTVPFPLRSA 377
          |||:|||:||||:||| :|:::: :  ||  :     ||||||| || ||| ||||||
Qy    121 GCHTQYMANMGSVASLALAIVVKGK--DS--S-----KLWGLVVGHHCSPRYVPFPLRYA 171

Db    378 CEFLMQVFGMQLNMEVELAAQLREK 402
          |||||| ||:|| ||::||:|| ||
Qy    172 CEFLMQAFGLQLQMELQLASQLAEK 196


RESULT   15
ID   P93524      PRELIMINARY;      PRT;   198 AA.
AC   P93524;
DT   01-MAY-1997 (TREMBLREL. 03, CREATED)
DT   01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT   01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
DE   PHYTOCHROME E (FRAGMENT).
GN   PHYE.
OS   SOPHORA AFFINIS.
OC   EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
OC   EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;
OC   FABALES; FABACEAE; PAPILIONOIDEAE; SOPHORA.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   LAVIN M., ESHBAUGH E., HU J.-M., MATHEWS S., SHARROCK R.A.;
RL   AM. J. BOT. 85:412-433(1998).
DR   EMBL; U78837; G1711110; -.
DR   PFAM; PF00360; phytochrome; 1.
DR   MENDEL; 14177; SOPaf;2331;mn14177.
KW   PHYTOCHROME.
FT   NON_TER       1      1
FT   NON_TER     198    198
SQ   SEQUENCE   198 AA;  22571 MW;  2A95C345 CRC32;

  Query Match           70.4%;  Score 1026;  DB 10;  Length 198;
  Best Local Similarity  81.0%;  Pred. No. 7.04e-234;
  Matches   132;  Conservative   19;  Mismatches  11;  Indels   1;  Gaps   1;

Db      1 YDRVMAYSFHEDDHGEVVSEIRRSDLEPLLPVLHYPATDIPQAARFLFQQNRVRMICDCH 60
          ||||| | ||||||||||||||||||||| |  |||||||||||||| ||||||||||:
Qy     35 YDRVMVYQFHEDDHGEVVSEIRRSDLEPYLG-LHYPATDIPQAARFLFKQNRVRMICDCN 93

Db     61 AKPVNVIQSEELRQPLCLVNSTLRSPLGCHTQYMANMGSIASLVMAVIVNGNDTTRLWGL 120
          | ||:|:|||||::|||||||||:| |||||||||||:||| :|::|:|:|:::|||| 
Qy     94 ATPVKVVQSEELKRPLCLVNSTLRAPHGCHTQYMANMGSVASLALAIVVKGKDSSKLWGL 153

Db    121 LVCHHTSPRYVPFPVRYACEFLMQAFGLQLYMEIQLASQMAEK 163
          :| || ||||||||:|||||||||||||| ||:|||||:|||
Qy    154 VVGHHCSPRYVPFPLRYACEFLMQAFGLQLQMELQLASQLAEK 196


Search completed: Mon Sep 13 14:24:39 1999
Job time : 35 secs.
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